

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 19:36:31 ; Search time 2746 Seconds

(without alignments)
10958.595 Million cell updates/sec

Title: US-09-976-605-5

Sequence: 1 aagcttcattgaataagtttaa.....agaagacggaaccctcgag 1034

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	991.6	95.9	144575	14 YD1293568	AD293568 Yaba-11ike
2	133.6	12.9	1023	6 ARI45601	ARI45601 Sequence
3	133.6	12.9	1023	6 IS8315	IS8315 Sequence 53
4	133.6	12.9	3567	14 SWPSPDH	I21931 Swinepox v1
5	133.6	12.9	14176	6 ARI45576	ARI45576 Sequence
6	133.6	12.9	14176	6 ARI45583	ARI45583 Sequence
7	133.6	12.9	14176	6 IS8290	IS8290 Sequence 1
8	133.6	12.9	14176	6 IS8297	IS8297 Sequence 14
9	133.6	12.9	14176	14 SWPHLSB	I22013 Swinepox v1
10	133.6	12.9	146454	14 AF410153	AF410153 Swinepox
11	133.6	12.9	146454	14 AF410153	AF410153 Swinepox
12	59.8	5.8	7218	6 AF6494	AF6494 Sequence 14
13	58.6	5.7	5420	3 AF056936	AF056936 Plasmodu
14	57.2	5.5	133501	2 AC116956	AC116956 Dictyoste
15	57	5.5	4102	3 AF270648	AF270648 Plasmodu
16	56.8	5.5	216508	10 AL683805	AL683805 Mouse DNA
17	55.4	5.4	1141	6 AX083744	AX083744 Sequence
18	54.8	5.3	914	3 PPRSA	X55124 P. falciparu
19	53.4	5.2	1141	6 AX083744	AX083744 Sequence
20	51.6	5.0	112698	2 AC119418	AC119418 Medicago
21	51.6	5.0	128096	2 AC126019	AC126019 Medicago
22	51.2	5.0	245802	2 AC006279	AC006279 Plasmodu
23	51.2	5.0	293431	2 PFMAL13P4	AL049181 Plasmodu
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26	50.2	4.9	82469	2 AC116330	AC116330 Dictyoste
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37	48.6	4.7	182025	9 AL138900	AL138900 Human DNA
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39	47.8	4.6	29016	2 AC117266	AC117266 Dictyoste
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41	47.6	4.6	4591	6 A00661	A00661 P. falciparu
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ALIGNMENTS

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RESULT 1
YD1293568/c
LOCUS YD1293568
DEFINITION Yaba-11ike disease virus (YLDV), complete genome.
ACCESSION AJ293568
VERSION AJ293568.1
KEYWORDS GI:12056159
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106L gene: 107L gene: 108L gene: 109L gene: 10L gene: 1173R gene:
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144R gene: 145R gene: 146R gene: 147R gene: 148R gene: 149R gene:
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Yaba-like disease virus.
Yaba-like disease virus.
Yabapoxvirus.
Yabapoxvirus, no RNA stage; Poxviridae; Chordopoxvirinae; Yabapoxvirus.
1 (bases 1 to 144575)
Lee, H.J.
Thesis (2000) Sir William Dunn School of Pathology, University of Oxford, Oxford, UNITED KINGDOM

2 (bases 1 to 144575)
Lee, H.J., Essani, K. and Smith, G.L.
The genome sequence of Yaba-like disease virus, a yatapoxvirus
Virology 281 (2), 170-192 (2001)

21176366
MEDLINE
11277691
PUBMED

REFERENCE
AUTHORS
TITLE
JOURNAL
UNITED KINGDOM

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2766 TTACACAGATCAGTTAGTACGAAATATCATATATACGAAAGTACACGAAACGT 2707
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Db 1865 1865 CC 1865

RESULT 2
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LOCUS ARI45601
DEFINITION Sequence 53 from patent US 6217882.
ACCESSION ARI45601
VERSION ARI45601.1 GI:15108790
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
Unclassified.
1 (bases 1 to 1023)
AUTHORS Moyer, R.W., Vinuela, E. and Gibbs, E.P.J.
TITLE Use of recombinant swine poxvirus as a live vaccine vector
JOURNAL Patent: US 6217882-A 53 17-APR-2001;
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Matches 451; Conservative 0; Mismatches 454; Indels 15; Gaps 3;

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324	---CGCTTCATTAAATCACTGGGTGTTATGAACAGAGATATATTTTGGTAGTAGGGT	380	GenBank	324
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681	CTCTGACGATTAATTAAGTGAATGAAGAAAGCAATTTTAAAGGTGAATTAATATATG	740	GenBank	681
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Accession	Source	Organism	Reference	Authors	Title	Journal	Medline	Pubmed	Reference
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621	CGGGTAAATGAGTATGAGATGTTAAACATGACTCTTGAATGCGAGTGAATTCATTTTACC	680							
13783	CAGAAATTTGAAGAGGAGA---TAATACATCAATTTGATATGACATTTTGAATATCAATTAAC	13839							
681	CTCTGACGATTAATTAAGTGAATGAAGAAAGAAACATTTTAAAGGTGAATTAATTAATG	740							
13840	CGCTGTCGGTCGCTGTTAAATGGTATATACATGAGAGACTTTGCTCCGAGTATTCGTTATG	13899							
741	TTAACGAGAACTACTATCCAGAAATGGGAGGAGAAATCCGATTAATGAGCCAGAGAGCCAG	800							
13900	ATTCG-----TAGTAAATGAATATGTTCTCTCGTAATACGAGATATCTCCGCGGTGAACCG	13953							
801	GTTTTCATGGAATATTAATAAAGATTAAGATGACAAACATATAGTTTACAGATTTAG	860							
13954	GATATCCGACTATTAACAGAGATTTAGGTGATTAATTTATTTTACATCAATCACTAGGG	14013							
861	TACGTACAACTCAAAAATGAGTAGTCAACTAGTATGTTGTTTCCATGACACTTTAG	920							
14014	TTATGTATCCAACTATATGTTCTTAATAGATAGCATGTGTGGATTTCAATAGTACGTTAG	14073							
921	AAGCGCAAGTTTAACTCTT	940							
14074	AACCAAGCATATATATGATG	14093							
RESULT 10									
AF410153	AF410153	146454 bp	DNA	linear	VRL 31-JAN-2002				
DEFINITION	Swinepox virus isolate 17077-99, complete genome.								
ACCESSION	AF410153								
VERSION	AF410153.1	GI:18448493							
KEYWORDS									
SOURCE	Swinepox virus.								
ORGANISM	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Sulipoxvirus.								
REFERENCE	1 (bases 1 to 146454)								
AUTHORS	Afonso, C.L., Tulman, E.R., Lu, Z., Zsak, L., Osorio, F.A., Balinsky, C.,								
TITLE	Kutish, G.F., and Rock, D.L.								
JOURNAL	The genome of swinepox virus								
MEDLINE	J. Virol. 76 (2), 783-790 (2002)								
PUBMED	21624277								
REFERENCE	11752168								
	2 (bases 1 to 146454)								

FEATURES	TITLE
source	AUTHORS Atonso,C.L., Tulman,E.R., Lu,Z., Ballinsky,C., Osorio,F.A., Zsak,L., Kutish,G.F. and Rock,D.L.
gene	Direct Submission Submitted (09-AUG-2001) African Swine Fever Research, Plum Island Animal Disease Center, U.S. Dept. Agriculture, Agricultural Research Service, P.O. Box 648, Greenvale, NY 11944-0848, USA
CDS	Location/Qualifiers 1..146454 /organism="Swinepox virus" /isolate="17077-99" /db_xref="taxon:10276" /note="Isolated from domestic swine in Hartington, Nebraska on March 12, 1999" complement(284..736) /gene="SPV001" complement(284..736) /gene="SPV001" /note="identical to SPV150, similar to lumpy skin disease virus LSDV001 and vaccinia virus strain Copenhagen B15R"
gene	/codon_start=1 /product="SPV001 A52R-like family protein" /protein_id="AAI69740.1" /db_xref="GI:18448494" /translation="METNYLYRNDFLDNDITFALDIYWSCISLRHDPAGKLFAV FEESRDRAEFVGENIIIEFYAKWELSHGFAFSKSWISTMLKENYIRSCAVGLL ARASTYGGDPERPSASTKYLLILKELLTDNDELKFKAIVALKRYG"
CDS	complement(811..1323) /gene="SPV002" complement(811..1323) /gene="SPV002" /note="identical to SPV149, similar to lumpy skin disease virus LSDV002"
gene	/codon_start=1 /product="SPV002 hypothetical protein" /protein_id="AAI69741.1" /db_xref="GI:18448495" /translation="MCALSTCTNRVFSGINGEVRGAIITYIVKEIGFIIFYLKSFOLL IDNIARIMLEIFVVDRLNLVIIGIYNMINEFPKKRIAFIFGNFNFDNYDIATKD DDMICQYFKDKDKDKDNNDIKSSNKTDMTNYDPAYDEFQVLNFETIPNPFK YTEHYKSGSK"
gene	complement(1430..2452) /gene="SPV003" complement(1430..2452) /gene="SPV003" /note="identical to SPV148" /codon_start=1 /product="SPV003 MHC class I alpha chain-like protein p32231"
CDS	/protein_id="AAI69742.1" /db_xref="GI:18448496" /translation="MITKAIVILSTITAYVDASAEFLVNTTYTLQDDNHRYDEFTDYI ENDILIKRKINSETGEDELNEPPTWEERKIYYPPNNNNFMFWLNRSKETSLETIN KLPEISNYKTMSLTIGTDLROLVNGGYTVAGNITRPDPKNKFFSRSTETPKR VTGMITVKSOHMERVMELHGSMTVLLDCPTADADYKISKGYIDKPVKPLVYGIERD NTYLICTPDNHRPSVAVKVYNIEDPADVDYDVYVNLLEDPTYLPGEGPYPIITERD LSDKLIETTSFRVWVPFITMSNRACVGHSLTEPSIYRCVNCSEPEVLYQGGRND LEDED"
gene	complement(2494..2772) /gene="SPV004" complement(2494..2772) /gene="SPV004" /note="identical to SPV147, similar to lumpy skin disease virus LSDV004"
CDS	/codon_start=1 /product="SPV004 hypothetical protein" /protein_id="AAI69743.1" /db_xref="GI:18448497" /translation="MLSYVINPLSTIVYFIIGNSKLLTYLMKIMFILRAVNPYSI ISNRGLSDSIINPFRKEKRRESFLSSIANPFRKETKKKGFGSGWG" complement(2821..3630) /gene="SPV005" complement(2821..3630) /gene="SPV005"

QY	801	GTTCCTTCAGTGAATTTTAAAAAGATTAAGTCAAAACACATATGTTTAACAGATTAG	860
Db	1647	GATATCCACATATTACTGAGAGATTAGGTGATAATATTATTATTCATCATCACCCTAGG	1588
QY	861	TACGTACAACATCAAAAATGAGTAGTCAACTAGATATGTTGTTTCCATGACACTTAG	920
Db	1587	TTATGTTACCAACTATCATCTGCTTATAGATAATAGCATGTGTGGATTTCATAGTACGTTAG	1522
QY	921	AAGCGCAAGTTTATPCTTGT	940
Db	1527	AAACCAAGCATATATGATGT	1508
RESULT 12			
166494/c			
LOCUS	166494	7218 bp	DNA linear PAT 28-DEC-1997
DEFINITION	Sequence 14 from patent US 5670367.		
ACCESSION	166494		
VERSION	166494.1	GI:2724471	
KEYWORDS			
SOURCE			
ORGANISM	Unknown.		
REFERENCE	Unknown.		
AUTHORS	Unclassified.		
TITLE	1 (bases 1 to 7218)		
JOURNAL	Donner, F., Schefflinger, F. and Falkner, F. Gunter.		
FEATURES	Recombinant fowlpox virus		
	Patent: US 5670367-A 14 23-SEP-1997;		
	Location/Qualifiers		
	1..7218		
	/organism="unknown"		
BASE COUNT	1944 a 1491 c 1486 g 1929 t	368 others	
ORIGIN			
Query Match	5.8%; Score 59.8; DB 6; Length 7218;		
Best Local Similarity	6.1%; Pred. No. 0.07; Mismatches 164; Indels 0; Gaps 0;		
Matches	25; Conservative 222;		
QY	623	GGAATGAGTTAGAGATGTAACATGACTGCTGTAATGACAGTAAATTCATTATACCT	682
Db	1460	GTTAAGAGATAGAAGCAATTGCTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	1401
QY	683	CCTGACGTAATTACTAGGTGATAGAAAACGAACTTTTAAAGTGAATATATAATATGTT	742
Db	1400	RR	1341
QY	743	AACGGAATACTATCCAGCAATGGGCGGAAAAATCCGATTATGAGCCGAGAGCCAGGT	802
Db	1340	RR	1281
QY	803	TTTCCATGGAATATTAATAAAGATTAAGATGCAACACATATATGTTTAAAGATTAGTA	862
Db	1280	RR	1221
QY	863	CGTACACATCAAAAATGAGTAGTCACTAGTATGTTGTTTCCATGACACTTAGAA	922
Db	1220	RR	1161
QY	923	GCGCAAGTTTACTCTGTTGGAAGAGATGCAATGAGAGCTATAGACACCTATATAGA	982
Db	1160	RR	1101
QY	983	AAACAGAGAAGAAGAGTGAAGAGATGACAGAGCGAAGAACCTTCGA	1033
Db	1100	RR	1050
RESULT 13			
AF056936			
LOCUS	AF056936	5420 bp	DNA linear INV 10-MAY-2001
DEFINITION	plasmodium falciplarium mature parasite-infected erythrocyte surface		
ACCESSION	AF056936		

[illegible]

Matches 218: Conservative 0; Mismatches 244; Indels 3; Gaps 1;

QY 559 ACATATCCAAAAGTAAAGTGAATACCAAGATACCAACCTACCTAGTGAAGT 618
 Db 4090 AGTTAAAAAGAGTAAAAAGAAATTAATTAATGAACCAAGATATATGTAGT 4149
 QY 619 AACGGTAAAGATTAAGATGTACATGACTCTTGAATGCAAGTGAATTCATTTA 678
 Db 4150 ACAGAAATTAATGACGAAAGATGTTAAACGAAAGATCCGAAAGCAAGATTAATGAT 4209
 QY 679 CCTCTACGCTAATTTCTTAAGTATAGAAAGCAACATTTAAAGCTCAATATAA 738
 Db 4210 AGAAAAAGAGTATATATAGAAAGTAAAGAAAGTAAAGTAAAGTAAAGTAA 4269
 QY 739 TGTAAACGAAATATCTATCCAGAAATGCGGAGAAATCCGATTTAGCCAGAGAGCC 798
 Db 4270 AGTTAAACAAAGAGTAAACAGAAATAGAAAAATGAAGAAAGATGCTATAGACA 4329
 QY 799 AGTTTTCATGGAATTTTAAAGATTAAGTGC---AAACACATATAGTTTAAACAGA 855
 Db 4330 AGAAATAGTAAAGCAAGAGTAAACGAAAGATACCAAAACACGATAAAGATAGG 4389
 QY 856 TTTTAGTACGTACACATCAAAATAGTCACTAGTATGTTGTTTCCATGACAC 915
 Db 4390 AAAAGAGTCAAAACCAATAGATGTTTAAAGAAAGAAAGATGACAGAAAGATC 4449
 QY 916 TTTAGAGCGCAAGTTTATCTGTTCTGAAGATGCAATGAGAGCTATACGACCCT 975
 Db 4450 TGAAGAGAGTCTGAAGAGAGTCTGAAGAGAACTGGAAGAGAGTCTGAAGAGATC 4509
 QY 976 ATATAGAAAAACAGAAAGAGAGAGTGAAGAGATGAGAGAGAGA 1020
 Db 4510 TGAAGAGAGTCTGAAGAGAGATCTGAAGAGAGTCTGAAGAGAGA 4554

RESULT 14

LOCUS AC116956 133501 bp DNA linear HTG 04-APR-2002
 DEFINITION Dictyostelium discoideum chromosome 2 map 1512060-1645559 strain
 AX4, *** SEQUENCING IN PROGRESS ***, in ordered pieces.

ACCESSION AC116956
 VERSION AC116956.1 GI:19919988
 SOURCE HTG: HTGS_PHASE2.
 ORGANISM Dictyostelium discoideum.
 REFERENCE Dictyostelium discoideum.
 AUTHORS Bukaiyola; Mycetozoa; Dictyostelidae; Dictyostelium.
 1 (bases 1 to 133501)
 Lehmann, R., Baumgart, C., Paria, G., April, J. F., Guigo, R., Kumpf, K.,
 Tunngal, B., Cox, E., Quail, M. A., Platzer, M., Rosenblatt, A. and
 Noegel, A. A.

TITLE Sequence and Analysis of Chromosome 2 of Dictyostelium
 JOURNAL Unpublished
 REMARK The Dictyostelium Genome Sequencing Consortium
 AUTHORS 2 (bases 1 to 133501).
 TITLE Direct Submission
 JOURNAL Submitted (04-APR-2002) Genome Analysis, Institute of Molecular
 Biotechnology, Beutenbergstr. 11, Jena 07745, Germany
 COMMENT CDS predictions from Geneid may contain errors. Further information
 is available from IMB Jena, Department of Genome Analysis
 (http://genome.imb-jena.de/dictyostelium/)
 and the University Cologne, Institute for Biochemistry I
 (http://www.uni-koeln.de/dictyostelium/project.shtml
 Funding
 Agency : Deutsche Forschungsgemeinschaft (DFG).
 * NOTE: This is a 'working draft' sequence.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.

FEATURES
 source
 1. 133501
 Location/Qualifiers
 /organism="Dictyostelium discoideum"

/strain="AX4"
 /db_xref="taxon:44689"
 /chromosome="2"
 /map="1512060-1645559"
 BASE COUNT 50753 a 15240 c 15399 g 51959 t 150 others
 ORIGIN

Query Match 5.5%; Score 57.2; DB 2; Length 133501;
 Best Local Similarity 44.0%; Pred. No. 0.13;
 Matches 379; Conservative 0; Mismatches 478; Indels 5; Gaps 3;

QY 17 TTAATATTTATTTACACAAATTTGAGCTTTGTAATGCTATCTTAATTAATTAAT 76
 Db 97394 TTTGTTTTTTTACAAATTTGGAAAAAGATTTGCAATGATCAAAACGTTAAAT 97335
 QY 77 ACTGTACGTTAAAGATTAATGAGTAAATGATGATGATGATGATGATGATGAT 136
 Db 97334 CCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 97275
 QY 137 CAGTTAGTAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 196
 Db 97274 TA-TTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 97216
 QY 197 GCTGATTTGTTTATTAATTTCTAGAGTCCCAACAGCGGATGATGATGATGAT 256
 Db 97215 ACTGATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 97156
 QY 257 TTTTGGTATCTTTATTAATGAAGAACTTTAGAAATTAATTAATTAATTAATTA 316
 Db 97155 TTTTATTTTATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 97096
 QY 317 ACTACTGCTTCATTAATTAATCACTGGGTGTTAAGAAAGATTTATTTTGGTAT 376
 Db 97095 AATTAATTAATTTACTATTAATTAATTAATTAATTAATTAATTAATTAATTA 97036
 QY 377 GGTATGTAGAAACGGCAAGCGATCCGTCAGATGATGATGATGATGATGAT 436
 Db 97035 GTGTGTTAAATTAATTAATTTTGGTGGGTGATGATTTTAAATTAATTAAT 96976
 QY 437 ACAGAAATGACACATTAAGTTTCCCAAGCTTGAATGTTTAACTGTTAAACCT 496
 Db 96975 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 96916
 QY 497 TGAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 556
 Db 96915 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 96856
 QY 557 TTAGATTACCAAAATGCTAAAGTGAATATCAAAAGATGCAACCTACAGTGA 616
 Db 96855 AATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 96798
 QY 617 GTACGGGTAAAGATTAAGATGATGATGATGATGATGATGATGATGATGAT 676
 Db 96797 TGAAGAGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 96738
 QY 677 TACCTCCGACGTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 736
 Db 96737 TACCTTATTTG--GTAAATTAATTAATTAATTAATTAATTAATTAATTA 96680
 QY 737 TATGTTACGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 796
 Db 96679 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 96620
 QY 797 CCAGGTTTCCATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 856
 Db 96619 TCTGATTTGAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 96560
 QY 857 TTAGTACGTACAAAGTCAAAA 878
 Db 96559 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 96538

RESULT 15

XX 11-OCT-2001; 2001WO-US32136.
 XX PR 11-OCT-2000; 2000US-239354P.
 XX PA (VIRION) VIRION THERAPEUTICS INC.
 XX PI McFadden G, Essani K;
 XX DR WPI: 2002-452345/48.
 XX P-PSDB: AAE23669.
 XX
 XX New Yatapoxvirus immunomodulatory polypeptide, gp38, useful for
 XX treating immunomodulatory disorders, e.g. cancer, transplant rejection,
 XX psoriasis, ischemic heart disease, atherosclerosis, or systemic lupus
 XX erythematosus
 XX
 XX Claim 18; Fig 4; 75pp; English.
 XX
 XX The present invention relates to novel Yatapoxvirus immunomodulatory
 XX peptides, gp38 and nucleic acid molecules encoding such proteins.
 XX Sequences of the invention are useful for treating immunomodulatory
 XX disorders such as cancers, tumors, inflammation, allergic reactions,
 XX transplant rejection, restenosis, antibody complex mediated diseases,
 XX autoimmune complications of AIDS (acquired immune deficiency syndrome),
 XX psoriasis, Behcet's syndrome, acute respiratory distress syndrome (ARDS),
 XX ischemic heart disease, type I insulin-dependent diabetes mellitus,
 XX Addison's disease, atherosclerosis or leukemia. They are also used in
 XX gene therapy. The present sequence is Tanapox virus (TPV) gp38 DNA.
 XX
 XX Sequence 1034 BP; 393 A; 147 C; 208 G; 286 T; 0 other:
 XX
 XX Query Match 100.0%; Score 1034; DB 24; Length 1034;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e-226;
 XX Matches 1034; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 541 ATGTCATTAGCTATTGTAGATTACCAAAAAATGGCTAAAGGTGAATACCAAAAAAGATAC 600
 YY AAGCTTCATGAAATGATTAATTTATTTAGCACAATTTGACAGTTGTGACTGATAC 60
 YY 1 AAGCTTCATGAAATGATTAATTTATTTAGCACAATTTGACAGTTGTGACTGATAC 60
 DB 61 TTTTAAATATTAATTTACTGTTAGCTTAAAGATAGGATGATGAGATTTTAA 120
 YY 61 TTTTAAATATTAATTTACTGTTAGCTTAAAGATAGGATGATGAGATTTTAA 120
 DB 61 TTTTAAATATTAATTTACTGTTAGCTTAAAGATAGGATGATGAGATTTTAA 120
 YY 61 TTTTAAATATTAATTTACTGTTAGCTTAAAGATAGGATGATGAGATTTTAA 120
 DB 121 CGATCATTTACAAAGATGATTAAGTAAGAAATATCATTAACACAGAACTAGACGG 180
 YY 121 CGATCATTTACAAAGATGATTAAGTAAGAAATATCATTAACACAGAACTAGACGG 180
 DB 121 CGATCATTTACAAAGATGATTAAGTAAGAAATATCATTAACACAGAACTAGACGG 180
 YY 121 CGATCATTTACAAAGATGATTAAGTAAGAAATATCATTAACACAGAACTAGACGG 180
 DB 181 AAACGTAATTTTAAAGGCTGATGATTTTAAATTTCTGAGAGTCCCAACAGCGGTA 240
 YY 181 AAACGTAATTTTAAAGGCTGATGATTTTAAATTTCTGAGAGTCCCAACAGCGGTA 240
 DB 181 AAACGTAATTTTAAAGGCTGATGATTTTAAATTTCTGAGAGTCCCAACAGCGGTA 240
 YY 181 AAACGTAATTTTAAAGGCTGATGATTTTAAATTTCTGAGAGTCCCAACAGCGGTA 240
 DB 241 CGATTCACACTTAACTTTTGGATCTTTAATGAAGAATCTTTAAGAAGAAATTAATA 300
 YY 241 CGATTCACACTTAACTTTTGGATCTTTAATGAAGAATCTTTAAGAAGAAATTAATA 300
 DB 241 CGATTCACACTTAACTTTTGGATCTTTAATGAAGAATCTTTAAGAAGAAATTAATA 300
 YY 241 CGATTCACACTTAACTTTTGGATCTTTAATGAAGAATCTTTAAGAAGAAATTAATA 300
 DB 301 AAACGATAGACAAAAAAGTACTGCTTCAATTAATCACTGGGTGTTAAGAAACAGATT 360
 YY 301 AAACGATAGACAAAAAAGTACTGCTTCAATTAATCACTGGGTGTTAAGAAACAGATT 360
 DB 301 AAACGATAGACAAAAAAGTACTGCTTCAATTAATCACTGGGTGTTAAGAAACAGATT 360
 YY 301 AAACGATAGACAAAAAAGTACTGCTTCAATTAATCACTGGGTGTTAAGAAACAGATT 360
 DB 361 AATATTTGGATGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 YY 361 AATATTTGGATGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 361 AATATTTGGATGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 YY 361 AATATTTGGATGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 421 AGGAGATTAAGGTTTACGAAATGACACATAAAGGTTTCCCAAGGTTGAATGTTAAC 480
 YY 421 AGGAGATTAAGGTTTACGAAATGACACATAAAGGTTTCCCAAGGTTGAATGTTAAC 480
 DB 421 AGGAGATTAAGGTTTACGAAATGACACATAAAGGTTTCCCAAGGTTGAATGTTAAC 480
 YY 421 AGGAGATTAAGGTTTACGAAATGACACATAAAGGTTTCCCAAGGTTGAATGTTAAC 480
 DB 481 TGTAAAAACACTCTTTGGAAGATGTAAAACTTCTAGAGGCTTTGAATACATGGG 540
 YY 481 TGTAAAAACACTCTTTGGAAGATGTAAAACTTCTAGAGGCTTTGAATACATGGG 540
 DB 481 TGTAAAAACACTCTTTGGAAGATGTAAAACTTCTAGAGGCTTTGAATACATGGG 540
 YY 481 TGTAAAAACACTCTTTGGAAGATGTAAAACTTCTAGAGGCTTTGAATACATGGG 540
 DB 541 ATGTCATTAGCTATTGTAGATTACCAAAAAATGGCTAAAGGTGAATACCAAAAAAGATAC 600
 YY 541 ATGTCATTAGCTATTGTAGATTACCAAAAAATGGCTAAAGGTGAATACCAAAAAAGATAC 600

DB 541 ATGTCATTAGCTATTGTAGATTACCAAAAAATGGCTAAAGGTGAATACCAAAAAAGATAC 600
 YY AAGCTTCATGAAATGATTAATTTATTTAGCACAATTTGACAGTTGTGACTGATAC 60
 YY 1 AAGCTTCATGAAATGATTAATTTATTTAGCACAATTTGACAGTTGTGACTGATAC 60
 DB 61 TTTTAAATATTAATTTACTGTTAGCTTAAAGATAGGATGATGAGATTTTAA 120
 YY 61 TTTTAAATATTAATTTACTGTTAGCTTAAAGATAGGATGATGAGATTTTAA 120
 DB 61 TTTTAAATATTAATTTACTGTTAGCTTAAAGATAGGATGATGAGATTTTAA 120
 YY 61 TTTTAAATATTAATTTACTGTTAGCTTAAAGATAGGATGATGAGATTTTAA 120
 DB 121 CGATCATTTACAAAGATGATTAAGTAAGAAATATCATTAACACAGAACTAGACGG 180
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 DB 121 CGATCATTTACAAAGATGATTAAGTAAGAAATATCATTAACACAGAACTAGACGG 180
 YY 121 CGATCATTTACAAAGATGATTAAGTAAGAAATATCATTAACACAGAACTAGACGG 180
 DB 181 AAACGTAATTTTAAAGGCTGATGATTTTAAATTTCTGAGAGTCCCAACAGCGGTA 240
 YY 181 AAACGTAATTTTAAAGGCTGATGATTTTAAATTTCTGAGAGTCCCAACAGCGGTA 240
 DB 181 AAACGTAATTTTAAAGGCTGATGATTTTAAATTTCTGAGAGTCCCAACAGCGGTA 240
 YY 181 AAACGTAATTTTAAAGGCTGATGATTTTAAATTTCTGAGAGTCCCAACAGCGGTA 240
 DB 241 CGATTCACACTTAACTTTTGGATCTTTAATGAAGAATCTTTAAGAAGAAATTAATA 300
 YY 241 CGATTCACACTTAACTTTTGGATCTTTAATGAAGAATCTTTAAGAAGAAATTAATA 300
 DB 241 CGATTCACACTTAACTTTTGGATCTTTAATGAAGAATCTTTAAGAAGAAATTAATA 300
 YY 241 CGATTCACACTTAACTTTTGGATCTTTAATGAAGAATCTTTAAGAAGAAATTAATA 300
 DB 301 AAACGATAGACAAAAAAGTACTGCTTCAATTAATCACTGGGTGTTAAGAAACAGATT 360
 YY 301 AAACGATAGACAAAAAAGTACTGCTTCAATTAATCACTGGGTGTTAAGAAACAGATT 360
 DB 301 AAACGATAGACAAAAAAGTACTGCTTCAATTAATCACTGGGTGTTAAGAAACAGATT 360
 YY 301 AAACGATAGACAAAAAAGTACTGCTTCAATTAATCACTGGGTGTTAAGAAACAGATT 360
 DB 361 AATATTTGGATGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 YY 361 AATATTTGGATGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 361 AATATTTGGATGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 YY 361 AATATTTGGATGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 421 AGGAGATTAAGGTTTACGAAATGACACATAAAGGTTTCCCAAGGTTGAATGTTAAC 480
 YY 421 AGGAGATTAAGGTTTACGAAATGACACATAAAGGTTTCCCAAGGTTGAATGTTAAC 480
 DB 421 AGGAGATTAAGGTTTACGAAATGACACATAAAGGTTTCCCAAGGTTGAATGTTAAC 480
 YY 421 AGGAGATTAAGGTTTACGAAATGACACATAAAGGTTTCCCAAGGTTGAATGTTAAC 480
 DB 481 TGTAAAAACACTCTTTGGAAGATGTAAAACTTCTAGAGGCTTTGAATACATGGG 540
 YY 481 TGTAAAAACACTCTTTGGAAGATGTAAAACTTCTAGAGGCTTTGAATACATGGG 540
 DB 481 TGTAAAAACACTCTTTGGAAGATGTAAAACTTCTAGAGGCTTTGAATACATGGG 540
 YY 481 TGTAAAAACACTCTTTGGAAGATGTAAAACTTCTAGAGGCTTTGAATACATGGG 540
 DB 541 ATGTCATTAGCTATTGTAGATTACCAAAAAATGGCTAAAGGTGAATACCAAAAAAGATAC 600
 YY 541 ATGTCATTAGCTATTGTAGATTACCAAAAAATGGCTAAAGGTGAATACCAAAAAAGATAC 600

RESULT 2
 AAD37917
 ID AAD37917 standard; DNA; 1017 BP.
 XX
 XX AAD37917;
 DT 10-SEP-2002 (first entry)
 XX
 XX Yaba-like disease virus (YLDV) gp38 DNA.
 DE
 XX Immunomodulatory disorder; gp38; cancer; inflammation; allergic reaction;
 XX tumour; transplant rejection; restenosis; autoimmune complication; AIDS;
 XX acquired immune deficiency syndrome; antibody complex mediated disease;
 XX psoriasis; Behcet's syndrome; acute respiratory distress syndrome; ARDS;
 XX ischemic heart disease; atherosclerosis; leukemia; Addison's disease;
 XX type I insulin-dependent diabetes mellitus; atherosclerosis; cytostatic;
 XX gene therapy; antibacterial; cardiac; vasotropic; virucide; YLDV;
 XX Yaba-like disease virus; gene; ds.
 OS
 XX Yaba-like disease virus.
 FH
 XX Key Location/Qualifiers
 FT 1..1017
 FT CDS /*tag= a
 FT /*product= "YLDV gp38 protein"
 XX
 XX WO200231115-A2.
 XX
 XX 18-APR-2002.
 XX
 XX 11-OCT-2001; 2001WO-US32136.
 XX
 XX 11-OCT-2000; 2000US-239354P.
 XX
 XX (VIRION) VIRION THERAPEUTICS INC.
 XX
 XX McFadden G, Essani K;

Query Match:	95.4%;	Score 986.6;	DB 24;	Length 1017;
Best Local Similarity	98.1%;	Pred. No. 8,9e-216;		
Matches 998; Conservative	0;	Mismatches 19;	Indels 0;	Gaps 0

OY	8	ATGATTAAGTAAATATTTATTTAGCAAAATGTAGACGTTTGTAACTGCATTAACCTTTAAAA	67
Db	1	ATGATTAAGTAACTATTATTATTAGCAAAATGTAGACGTTTGTAACTGCATTAACCTTTAAAA	60
OY	68	TATTAATTAACCTGTACGTTAAAGATATAGGGTATACGATGAGATTTTACGATCAT	127
Db	61	TATTAATTAACCTGTACGTTAAAGATATAGGGTATACGATGAGATTTTACGATCAT	120
OY	128	TACAACATAGATTACTAATACGAAATATACATATACACGAAACTAGACACGAAACGTA	187
Db	121	TACAACATAGATTACTAATACGAAATATACATATACACGAAACTAGACACGAAACGTA	180
OY	188	AAATTTAGGGCGTATGTTGTTAAATATTTCTATAGAGATCCCAACACGCGAGTTACGATTAC	247
Db	181	AAATTTAGGGCGTATGTTGTTAAATATTTCTATAGAGATCCCAACACGCGAGTTACGATTAT	240
OY	248	AACCTTAACCTTTGGATATCTTTTAATGAAACAACTTTAGAGAATTTAATATTAACAAACGAT	307
Db	241	AACCTTAACCTTTGGATATCTTTTAATGAAACAACTTTAGAGAATTTAATATTAACAAACGAT	300
OY	308	AGCACAAAACATCACTCCCTTCATTAATCACTGGGGTATGATAAACACAGATTATTATTT	367
Db	301	AGCACAAAACATCACTCCCTTCATTAATCACTGGGGTATGATAAACACAGATTATTATTT	360
OY	368	GGTAGTTATGGGTATGTAGAAAACGGCCAAAGGACCGTTGGCCGATACCATACAGAGAT	427
Db	361	GGTAGTTATGGGTATGTAGAAAACGGCCAAAGGACCGTTGGCCGATACCATACAGAGAT	420
OY	428	AAAAGGTTACGAAATATACACATTAAGGTTTCCCAAGGTTGGAAATGTTAACTGTAAAA	487
Db	421	AAAAGGTTACGAAATATACACATTAAGGTTTCCCAAGGTTGGAAATGTTAACTGTAAAA	480
OY	488	AAACACTCTTTGGAAAGATGTAAAAACTATCTATAGCGGTTTGGATATACATGGGAGGTCA	547
Db	481	AAACACTCTTTGGAAAGATGTAAAAAGCTATTATTAGCGGTTTGGATATATAGGAGATGTCA	540
OY	548	TTAGCATTTTATAGATTACCAAAAAATGGCTAAAGGTGAAATACCAAAAGATACAACACT	607
Db	541	TTAGCATTTTATAGATTACCAAAAAATGGCTAAAGGTGAAATACCAAAAGATACAACACT	600
OY	608	ACAAGTAAAGTAAACGGGTAAATGAGTTAGAGATGATTAACATATACCTTTGAAATGCAAGTGA	667
Db	601	ACAAGTAAAGTAAACGGGTAAATGAGTTAGAGATGATTAACATATACCTTTGAAATGCAAGTGA	660

OY	668	AATTCATTTTAACCCCTCGTACGTAATTACTTAAGTGGATGAAAGCGAACATTTTAAAGGT	727
Db	661	AATTCATTTTAAACCCTCGTACGTAATTACTTAAGTGGATGAAAGCGAACATTTTAAAGGT	722
OY	728	GAATATTAATAATGTGTTAAACGGAACATCTCTCCAGAAATGGGGGAGAAAATCCGATTATGAG	787
Db	721	GAATATTAATAATGTGTTAAACGGAACATCTCTCCAGAAATGGGGGAGAAAATCCAAATTATGAG	780
OY	788	CCAGGAGAGCCAGGTTTTCATGGAATTTTAAAAAAGATTAAGATCCAAACACATATAGT	847
Db	781	CCAGGAGAGCCAGGTTTTCATGGAATTTTAAAAAAGATTAAGATCCAAACACATATAGT	840
OY	848	TTAAACGATTTACTAGTACACATCATATAAATGAAGTACTCACTAGTATGTGTGTTTC	907
Db	841	TTAAACGATTTACTAGTACACATCATATAAATGAAGTACTCAACGATATGTGTGTTTC	900
OY	908	CATGACACTTTAAGACGCAAGTTTATCTTTGTGAGAGATCCATATGAGAGACTTTAC	967
Db	901	CATGACACTTTAAGACGCAAGTTTATCTTTGTGAGAGATCCATATGAGAGACTTTAC	960
OY	968	GACCACTTATATGAAAAACAGAAAGAGAGAGGTGAAGAGATGGAAGAAGAGCGA	1024
Db	961	GATCACCCTATATGAAAAACAGAAAGAGAGAGGTGAAGAGATGGAAGAAGAGCTGA	1017

RESULT 3	
AAD37946	
ID	AAD37946 standard; DNA; 1183 BP.
XX	

DT 10-SEP-2002 (first entry)
XX

DE 100 monkey tumor virus (YMTV) gp38 DNA
XX

KW immunosuppression; disorder; gp38; cancer; inflammation; allergic reaction
KW tumour; carcinoma; cancer; virus; virus; virus; virus; virus; virus; virus
KW acquired; transplant; rejection; testotoxic; autoimmune complication; AIDS;
KW acquired; immune deficiency syndrome; antibody complex mediated disease;
KW psoriasis; Behcet's syndrome; acute respiratory distress syndrome; ARDS;
KW ischaemic heart disease; atherosclerosis; leukemia; Addison's disease;
KW type I insulin-dependent diabetes mellitus; leukoencephalitis; cytostatic;
KW gene therapy; antibacterial; cardiant; vasotropic; virucide; YMWV;
KW Yaba monkey tumor virus; gene; ds.
OS Yaba monkey tumor virus.
XX

EH	Key	Location/Qualifiers
FT	CDS	1..183

```

FT      /product= "MYT1 gp38 partial protein"
FT      /transl_except= (pos:166..168, aa:lys)
FT      /transl_except= (pos:169..171, aa:arg)
FT      /note= "CDS does not include stop codon"
FT      /partial

```

PN W0200231115-A2

PD 18-APR-2002

11-OCT-2001; 2001WO-US32136

PR 11-OCT-2000; 2000US-239354P
YY

PA (VIRO-) VIRON THERAPEUTICS INC.
XY

Pl McFadden G, Essani K;
XX

DR WP1: 2002-452345/48.
DR P-PSDB: AAFF23668

PT New Yatanovirus

new immunomodulatory polypeptide, gp38, useful for treating immunomodulatory disorders, e.g. cancer, transplant rejection asthma, ischemic heart disease, atherosclerosis, or systemic lupus

CC The present invention relates to novel tatapoxvirus immunomodulatory
CC peptides, gp38 and nucleic acid molecules encoding such proteins.
CC Sequences of the invention are useful for treating immunomodulatory
CC

[illegible]

PF 06-APR-2001; 2001WO-EP03971.
 XX
 PR 06-APR-2000; 2000DE-1019058.
 PR 07-APR-2000; 2000DE-1019173.
 PR 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2002-017471/02.
 XX
 PT New nucleic acid sequences from chemically modified genes associated
 with DNA replication, useful for analysing cytosine methylations for
 diagnosis and therapy of diseases e.g. Ataxia telangiectasia
 XX
 PS Claim 1; SEQ ID NO 49; 23pp + Sequence Listing; English.
 XX
 CC The invention relates to nucleic acid sequences comprising at least 18
 CC bases of a chemically pretreated gene associated with gene regulation,
 CC selected from 94 genes (AB149301-AB149394) and/or complementary sequences
 CC associated with DNA replication, CENPB, DNAB2, ATR, CHD1L, ERCC3, SRRP1,
 CC RAD50 and Lig2. The chemical pretreatment converts cytosine bases
 CC unmethylated at the 5-position to uracil or another base with
 CC hybridisation behaviour dissimilar to cytosine, to enable analysis of
 CC cytosine methylations. The DNA sequences and method are useful in the
 CC diagnosis of diseases (or predisposition to diseases) associated with DNA
 CC replication and in therapy of such diseases, by enabling analysis of the
 CC cytosine methylation patterns of such genes. They are especially useful
 CC in diagnosis and therapy of e.g. Ataxia telangiectasia, ATR-X, Bloom's
 CC syndrome, solid tumours and cancer.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification and was supposed to be available directly from WIPO at
 CC ftp.wipo.int/pub/published/pct_sequences. However, the sequence data did
 CC not correspond to that referred to in the specification. The present data
 CC is taken from EPO data for the patent.
 CC
 XX
 SQ Sequence 6306 BP; 1957 A; 172 C; 1320 G; 2857 T; 0 other;
 Query Match 4.9%; Score 51; DB 24; Length 6306;
 Best Local Similarity 44.4%; Pred. No. 0.043;
 Matches 260; Conservative 0; Mismatches 315; Indels 10; Gaps 1;
 QY 442 AATGACACATAAAGGTTTCCCAAGGTGGATGTTAACTGTAATAAAACACCTCTTGAA 501
 DB 548 AATATATTTAAAGATTAAGTAACTGTAATTTGATTAATAATTTATATAGTTTGTGAA 607
 QY 502 AGATGTAATAAAGTCTTACGCGTTTGAATACAGGATGTTCAATTTGCTATTGTA 561
 DB 608 ATTTATTAAGTTATTTATTTATTAAGAGTAAGATTAATAATTAATTAAGATATTTTCG 667
 QY 562 TTACCAAAAATGCGTAAAGTAAATVACCAAAAGATACCAACCTACAGTGAAGTAAC 621
 DB 668 AGATATATAGTTTATGATTTAAAGTTATGATATATTTTAAAGAAAATAGGTAG 727
 QY 622 GGGTAATAGCTTAGAAGATGTAACATGACTCTGTAAGCAGTGTAAATTCATTTCACC 681
 DB 728 TGGTTTAGGATGAAAAAATAGATTTATAGATTAATGATTTTATATATATTTGTA 787
 QY 682 TCTGACGTAATTAATGATGATAGTAAGACCAATTTTAAAGGTAATATATATGCT 741
 DB 788 TTTAAGGTGATTAAGTAAAGGTGTAATAAGTATAGTAAATTAATTAAGATTAAT 847
 QY 742 TAACGGAAGTACTATCCAGATGGGAGAAAATCCGATTATGACCCAGAGACGAG 801
 DB 848 GAAATTAATAATTAATAGATGAGATTTATTTGATATATATATGAGAGTGAATTT 907
 QY 802 TTTTCCATGGAATATTTAAAAAGATTAAGTCAAAACATATATAGTTTAAACAGATTAG 861
 DB 908 TAGATGACGATTTATTAATATGAAAGCTAAATTTTAAATATTTTAAAGAAAAATGAAT 967
 QY 862 ACGTACACATCAAAAAATGATGATCACTAGTATGTTGTTTCCATGACACTTTAGA 921

DB 968 ATTTTAAGCTAGCATGATTAATAAGATTTAATAAGATTTTATGATTTT--- 1024
 QY 922 AGCGCAAGTTTATCTGTTCTGAAAGATGCAATGAGACCTATACACCACTATATAG 981
 DB 1025 -----TTTATATTTAATTTAAAGGGGAAAAGTTTATTTATTTAAAAAGAGTTT 1077
 QY 982 AAAAAGACAGAGAGAGAGAGTGAAGAGCATGAAGAAGAGGAAA 1026
 DB 1078 TTAATTAATAAAAAAAGATGATGATGAAGAGAGAGAGGAAA 1122
 RESULT 10
 AA087587
 ID AA087587 standard; DNA; 1686 BP.
 XX
 AC AA087587;
 XX
 DT 19-DEC-1995 (first entry)
 XX
 DE DNA encoding Leucocytozoon protozoan structural protein epitope.
 XX
 DE Leucocytozoon protozoan; structural protein; epitope; vaccine; fowl;
 KW Leucocytozoonosis; treatment; ss.
 OS Leucocytozoon protozoa sp.
 XX
 PN JP07089995-A.
 XX
 PD 04-APR-1995.
 XX
 PF 10-SEP-1993; 93JP-0226078.
 XX
 PR 10-SEP-1993; 93JP-0226078.
 XX
 PA (DOBU-) DOBUTSUO SEIBUTSUGAKUTERI SEIZAI KYOKAI.
 PA (NISS-) NISSEIKEN KK.
 XX
 DR WPI; 1995-167252/22.
 DR P-PSDB; AAR70491.
 XX
 PT Immune inducing polypeptide against Leucocytozoon protozoa - useful
 PT in production of vaccines for treatment of Leucocytozoonosis in
 PT fowl.
 PS
 PS Claim 1; Page 12-14; 20pp; Japanese.
 CC AA087587-89 encode polypeptides having a whole or partial epitope of a
 CC structural protein of Leucocytozoon protozoa (see AAR70491-93). The
 CC polypeptides and DNA encoding them are useful in the production of
 CC vaccines for the treatment of Leucocytozoonosis of fowl.
 CC
 XX
 SQ Sequence 1686 BP; 915 A; 129 C; 382 G; 260 T; 0 other;
 Query Match 4.8%; Score 49.4; DB 16; Length 1686;
 Best Local Similarity 47.1%; Pred. No. 0.076;
 Matches 152; Conservative 0; Mismatches 171; Indels 0; Gaps 0;
 QY 706 ACAAAGCGAATTTTAAAGTGAATTAATATGTTTAAAGGATATCTTCAGATG 765
 DB 210 ABAAGAGAGAGATGAG 269
 QY 766 GGGGGAATAATCCGATTATGAGCCAGAGAGCCAGTTTCCATGGAATTTAAAAAGA 825
 DB 270 AGAAG 329
 QY 826 TAAAGATGCAACACATATAGTTTAAAGATTTAGCTTACATCAATCAATCAATGAGTAG 885
 DB 330 ACAAGATGAAGTGAAG 389
 QY 886 TCAATGATAGTGTGTTTCCATGACACTTTGAGACCGCAAGTTTATCTTCTGCA 945
 DB 390 TGAAG 449

FT exon 1199..4225
 FT /*tag- b
 PN MO8601802-A.
 XX 27-MAR-1986.
 PD 11-SEP-1985; 85WO-0006960.
 XX 11-SEP-1984; 84AU-0007067.
 PR 11-SEP-1984; 84AU-0007066.
 PR 10-SEP-1985; 85AU-0047326.
 XX (HALL-) HALL INST MED RES.
 PA
 PI Kemp DJ, Anders R, Coppel RL, Brown G, Saint RB, Cowman AF;
 XX WPI: 1986-094065/14.
 DR P-PSDB; AAP60569.
 XX
 PT DNA coding for Plasmodium falciparum antigens - expressing
 PT poly-peptide(s) having antigenicity of RESA or FIRA antigens of P
 PT falciparum
 XX
 PS Claim 4; Fig 1; 55pp; English.
 CC The inventors claim a novel DNA molecule which comprises a
 CC nucleotide sequence coressp. to all or a portion of the base
 CC sequence coding RESA (AAN60472) or FIRA (AAN60473). RESA and FIRA have
 CC antigenicity suitable for providing protective immunity against
 CC Plasmodium falciparum malarial infections.
 CC
 SQ Sequence 4590 BP; 1933 A; 437 C; 673 G; 1547 T; 0 other;
 Query Match 4.6%; Score 47.6; DB 7; Length 4590;
 Best Local Similarity 44.1%; Pred. No. 0.24;
 Matches 200; Conservative 0; Mismatches 254; Indels 0; Gaps 0;
 QY 569 AAAATGGCTAAAGGTAATACCAAAAGATACACACCTAGAGTGAAGTAAAGGATAT 628
 DB 3635 AAAAACCAAAATGAAATGTACCAAGACATGTAACAATATGCTGAAGAAATGTAGAA 3694
 QY 629 GAGTTAGAGATGCTACATGACTCTTGAATGACAGTAAATTCATTTACCTCTCTGAC 688
 DB 3695 CATGATGCTGAAGAAATGTAGAACATGATGCTGAAGAAATGTGAACATGATCTGAA 3754
 QY 689 GTAAATCTAGTGTAGTAAAGCGAACATTTTAAAGTGAATATTAATATGTAAACGA 748
 DB 3755 GAAATGTAGACATGATGCTGAAGAAATGTAGAACATGATGCTGAAGAAATGTAGAA 3814
 QY 749 AGATTAATCCAGAAATGGGGAGAAATCCGATTAATGAGCCAGAGAGCCAGTTTCCA 808
 DB 3815 GAAATGTTGAAGAAATGTAGAAAGAAATGTAGAAAGAAATGTAGAAAGAAATGTAGAA 3874
 QY 809 TCGAATATTTAAAGATTAAGATGCAACATATAGTTTAAAGATTTAGTACTAGCA 868
 DB 3875 AATGTTGAAGAAATGTAGAAAGAAATGTAGAAAGAAATGTAGAAAGAAATGTAGAAAGAAAT 3934
 QY 869 ACATCAAAATGAGTAGTCACTAGTATGTTGTTTCCATGACACTTTAGAACGCA 928
 DB 3935 GTTGAAGAAATGTAGAAAGAAATGTAGAAAGAAATGTAGAAAGAAATGTAGAAAGAAAT 3994
 QY 929 GTTTAACTGTTCTGAAGATGCAATGAGAGCTATAGCACCCTATATGAAAGCA 988
 DB 3995 GTTGAAGAAATGTAGAAAGAAATGTAGAAAGAAATGTAGAAAGAAATGTAGAAAGAAATGT 4054
 QY 989 GAAGAAGAGAGTGAAGAGATGAGAGAGAG 1022
 DB 4055 GAAGAAGAAATGTAGAAAGAAATGTAGAAAGAAATG 4088

ID AAT05868 standard; DNA; 3399 BP.
 AC AAT05868;
 XX
 XX 14-AUG-1996 (first entry)
 DT
 XX
 XX Chicken leucocytozoan DNA encoding immunogenic protein for vaccines.
 DE
 XX
 XX Chicken leucocytozoan; immunogen; recombinant vaccine; protection;
 KW Immunisation; vaccination; ss.
 XX
 XX Chicken leucocytozoan.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 1..3399
 FT /*tag= a
 FT misc-feature 1150..3218
 FT /*tag= b
 FT /note= "fragment referred to in the claims, for
 FT use as insert in a recombinant vaccine
 FT against chicken leucocytozoan disease"
 XX
 PN JP07284392-A.
 PD 31-OCT-1995.
 XX
 PD 19-APR-1994; 94JP-0080643.
 XX
 PF 19-APR-1994; 94JP-0080643.
 XX
 PR 19-APR-1994; 94JP-0080643.
 XX
 PA (DOBU-) DOBUTSUVO SEIBUTSUGAKUTEKI SEIZAI KYOKAI.
 PA (KITA) KITASATO KENKYUSHO SH.
 XX
 DR WPI: 1996-006311/01.
 DR P-PSDB; AAR97866.
 XX
 XX Chicken leucocytozoan immunogenic protein - used in a recombinant
 PT vaccine against chicken leucocytozoan disease
 PT
 PS Claim 6; Page 6-9; 35pp; Japanese.
 CC AAT05868 encodes a chicken leucocytozoan immunogenic protein, this DNA
 CC or a fragment of it can be used in a recombinant vaccine to immunise
 CC against chicken leucocytozoan disease. The DNA is used in a vector
 CC and operatively linked to an expression regulatory sequence as in
 CC standard practice.
 SQ Sequence 3399 BP; 1577 A; 508 C; 798 G; 516 T; 0 other;
 Query Match 4.6%; Score 47.2; DB 17; Length 3399;
 Best Local Similarity 43.8%; Pred. No. 0.28;
 Matches 205; Conservative 0; Mismatches 263; Indels 0; Gaps 0;
 QY 559 AGATTACCAAAATGCTAAAGTGAATACCAAAAGATACACACCTAGTGAAGT 618
 DB 2601 AGAAGAAAGAAAGAAAGTAAACATGTAAGAAAGAAAGTAAACATGTAAGAAAGAAAG 2660
 QY 619 AACGGTAATGAGTGAAGATGTAACATGACTCTTGAATGAGTGAATTAATCATTTTA 678
 DB 2661 AAAAGTAAACATGTAAGAAAGAAAGAAAGTAAATCATGAAAGAAAGAAAGAAAGAAAG 2720
 QY 679 CCTTCCTGACGTAATTAATTAAGTGAATGAAGCAACATTTTAAAGTGAATTAATAA 738
 DB 2721 TGAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2780
 QY 739 TGTTAAGGAAGATACATCTTCCAGATGGGGAGAAATCCGATTTAGAGCCAGAGAGCC 798
 DB 2781 AGAGGAAGAAAGAAAGAAAGAAAGATGAGGAAGGAAGAAAGAAAGAAAGAAAGAAAG 2840
 QY 799 AGGTTTCATGATGATTTAAAGAAAGATTAAGATGCAACATATAGTTTAACAGATT 858
 DB 2841 AGAAGAAAGAAAGAAATTAAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGT 2900

OY		859	AGTAGGTACAAATCAAAAATGATAGTACACTAGTAATGTTGGTTTCATGCACCTTT	918
DB		2901	AACACATGAAGAAGAAAGAAAAAGTAAACACATGAAGAAGAAAAAGTAAACACATCA	2966
OY		919	AGAACGCCAAGTATTACTTGTTTCGAAGATGCATGACAGCGTAAACGACCACCTATA	978
DB		2961	AGAAAGMAAATAATGTACATATGAAAGAAAGMAAAGMAAAGTAAACATGAAAGAAAGA	3026
OY		979	TAGAAAAACAGAGAAGGCAAGGTCGAAGAGAGATGAAGAGCGGAAA	1026
DB		3021	AAAAGTAAACACATGAAAGAAAGAAAAAGTAAACACATGAAAGAAAGA	3068
 RESULT 14 ABL/70327/C ID ABL/70327 standard; DNA: 6012 BP. XX ABL70327: XX XX ABL70327: XX XX 01-JUN-2002 (first entry) XX XX Chemically treated cell signalling DNA sequence#109. XX XX Cell signalling; cytosine methylation; cell signalling disease; XX cancer; tumour; cytostatic; ds. XX XX Unidentified. XX XX WO200202807-A2. XX XX PD 10-JAN-2002. XX XX PF 29-JUN-2001; 2001WO-EP07471. XX XX PR 30-JUN-2000; 2000DE-1032529. XX PR 01-SEP-2000; 2000DE-1043826. XX XX PA (EPIC-) EPIGENOMICS AG. XX XX PI Olek A, Piepenbrock C, Berlin K; XX DR WPI; 2002-154758/20. XX PT Nucleic acid, useful for diagnosis and therapy of diseases associated PT with cell signalling e.g. cancer, comprises chemically modified genomic PT sequences of genes associated with cell signalling - PT XX XX Claim 1; SEQ ID NO 217; 24pp+sequence listing; English.				

The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as oligonucleotides and/or PNA-oligomers for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling.

Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.

SQ		Sequence 6012 BP; 1785 A; 32 C; 958 G; 3237 T; 0 other;
 Query Match 4.5%; Score 47; DB 24; Length 6012; Best Local Similarity 51.2%; Pred. No. 0.35; Matches 110; Conservative 0; Mismatches 105; Indels 0; Gaps 0;		
OY	414	ACCATATCAGGAGATAAAGTTTACGAAATATGACACATTAAGGTTTTCCCAAGTTGGAA 473

Dd		4716 AACATAAAAAACTTATAAAAACCTATTGTAATTTAATCTGTCTTAATTTTTAA	4657
Oy		474 TGGTAAGTGTAATAAACACGTCCTTGGAAAGTGTAAAAACTATCTAGCGGCTTTGCAT	533
Dd		4656 TCTTAAAAAAAAAAAAAAAAAATATAAAAAATAATCACTAATATTAATTATTTGATA	4597
Oy		534 ACATGGGATGTCCTCATTTAGCTATTTTAGTTCACAAAAAATGGTAAAGGTGAATACCAC	593
Dd		4596 AATAAACAATTTCATTATTTTAATCCTACCTACACAAAACAATAATAAAAAACTTCTACCA	4537
Oy		594 AAGATACACACAGCTACAGTGAAGTAACGGTAAT	628
Dd		4536 TAACATAAAACCCACCTTATATAAAAAATTTTCAT	4502
RESULT 15			
AAS61274/C			
ID	AAS61274 standard; DNA; 6012 BP.		
XX			
XX	AAS61274;		
DE			
DT	29-JAN-2002 (first entry)		
XX			
DE	Human gene regulation-associated gene oligonucleotide #229.		
XX			
KW	Human; Gene regulation-associated gene; severe combined immunodeficiency;		
KW	cardiac damage; inflammatory response; Haemophilia; Werner syndrome;		
KW	asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome;		
KW	renal disease; Preeclampsia; cardiac allograft vascular disease;		
KW	colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour;		
KW	immunostimulant; cardiacant; antiinflammatory; coagulant; antisthmatic;		
XX	nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.		
KM	Homo sapiens.		
OS			
PX	WO200177375-A2.		
FN			
XX			
PD	18-OCT-2001.		
XX			
PF	06-APR-2001; 2001WO-EP03968.		
XX			
PR	06-APR-2000; 2000DE-1019058.		
PR	07-APR-2000; 2000DE-1019123.		
PR	30-JUN-2000; 2000DE-1032529.		
PR	01-SEP-2000; 2000DE-1043826.		
XX			
PA	(EPIG-) EPIGENOMICS AG.		
XX			
PI	Olek A, Piepenbrock C, Berlin K;		
DR	WPI; 2002-017470/02.		
PT			
PT	New nucleic acid sequences from chemically modified genes associated		
PT	with gene regulation, useful for analysing cytosine methylations for		
PT	diagnosis and therapy of diseases e.g. severe combined immunodeficiency		
PT	disease -		
PS			
PS	Disclosure; SEQ ID NO 235; 26pp; English.		
XX			
XX	The invention relates to 224 nucleic acid sequences comprising at least		
CC	18 bases of a chemically pretreated gene associated with gene regulation		
CC	selected from 43 known genes (or complementary sequences). The		
CC	chemical pretreatment converts cytosine bases unmethylated at the		
CC	5-position to uracil or another base with hybridisation behaviour		
CC	dissimilar to uracil or another base with hybridisation behaviour		
CC	The DNA sequences, oligomers (or sets/arrays) and method are		
CC	useful in the diagnosis of diseases (or predisposition to diseases)		
CC	associated with gene regulation and in therapy of such diseases, by		
CC	enabling analysis of the cytosine methylation patterns of such genes,		
CC	kits are provided. They are especially useful in diagnosis		
CC	and therapy of e.g. severe combined immunodeficiency disease, cardiac		
CC	disorders, haemophilia, solid tumours and cancer, Werner syndrome,		
CC	C		

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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 20:17:01 ; Search time 78 Seconds
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	133.6	12.9	1023	1 US-08-307-499-53	Sequence 53, Appl
2	133.6	12.9	1023	4 US-09-299-268-53	Sequence 53, Appl
3	133.6	12.9	14176	1 US-08-307-499-1	Sequence 1, Appl
4	133.6	12.9	14176	1 US-08-307-499-14	Sequence 14, Appl
5	133.6	12.9	14176	4 US-09-299-268-1	Sequence 1, Appl
6	133.6	12.9	14176	4 US-09-299-268-14	Sequence 14, Appl
7	59.8	5.8	7218	1 US-08-232-463-14	Sequence 14, Appl
8	42	4.1	1956	4 US-08-559-8968-1	Sequence 1, Appl
9	40.6	3.9	4163	4 US-09-004-838-70	Sequence 70, Appl
10	40.2	3.9	663	4 US-08-998-416-191	Sequence 191, Appl
11	39.4	3.8	662	4 US-08-998-416-185	Sequence 185, Appl
12	39	3.8	711	4 US-08-998-416-786	Sequence 786, Appl
13	39	3.8	724	4 US-08-998-416-683	Sequence 683, Appl
14	39	3.8	732	4 US-08-998-416-1036	Sequence 1036, Appl
15	39	3.8	828	4 US-08-998-416-538	Sequence 538, Appl
16	38.4	3.7	1158	4 US-09-134-001C-851	Sequence 851, Appl
17	38.2	3.7	19124	2 US-08-487-826B-13	Sequence 13, Appl
18	37.6	3.6	834	4 US-08-998-416-305	Sequence 305, Appl
19	37.2	3.6	665	4 US-08-998-416-937	Sequence 937, Appl
20	37.2	3.6	4285	4 US-09-410-464-1	Sequence 1, Appl
21	37	3.6	3808	2 US-08-417-210A-79	Sequence 79, Appl
22	36.8	3.6	1431	4 US-09-134-001C-1621	Sequence 1621, Appl
23	36.6	3.5	701	4 US-08-998-416-701	Sequence 701, Appl
24	36.6	3.5	854	4 US-08-998-416-534	Sequence 534, Appl
25	36.6	3.5	860	4 US-08-998-416-287	Sequence 287, Appl
26	36.6	3.5	14507	3 US-08-785-150-1	Sequence 1, Appl
27	36.6	3.5	14507	4 US-09-660-299-1	Sequence 1, Appl

28	36.6	3.5	14507	4 US-09-435-377-1	Sequence 1, Appl
29	36	3.5	658	4 US-08-998-416-595	Sequence 595, Appl
30	36	3.5	3891	1 US-08-480-604A-27	Sequence 27, Appl
31	36	3.5	3891	2 US-08-405-496A-27	Sequence 27, Appl
32	36	3.5	3891	4 US-08-915-136-27	Sequence 27, Appl
33	35.8	3.5	2075	1 US-08-238-163-3	Sequence 3, Appl
34	35.6	3.4	84495	4 US-09-797-906-3	Sequence 3, Appl
35	35.4	3.4	986	4 US-09-072-596-334	Sequence 334, Appl
36	35.4	3.4	3395	4 US-09-103-478-3	Sequence 3, Appl
37	35.4	3.4	3395	4 US-09-193-931C-3	Sequence 3, Appl
38	35.4	3.4	5181	1 US-08-257-073-10	Sequence 10, Appl
39	35.4	3.4	5470	1 US-08-441-139-12	Sequence 12, Appl
40	35.4	3.4	5470	6 5196523-5	Patent No. 5196523
41	35.4	3.4	7560	4 US-09-103-478-4	Sequence 4, Appl
42	35.4	3.4	7560	4 US-09-193-931C-4	Sequence 4, Appl
43	35.2	3.4	1194	4 US-08-929-329-3	Sequence 3, Appl
44	35	3.4	1236	2 US-08-741-134-5	Sequence 5, Appl
45	35	3.4	4766	5 PCT-US93-07261-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-307-499-53
Sequence 53, Application US/08307499
Patent No. 5651972
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
NUMBER OF SEQUENCES: 60
TITLE OF INVENTION: Live Vaccine Vector
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,499
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1023 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

||||| 215 TTAAGAGAGCTAGTATGATATTTTCGAAAAATATATATTTATGTTCTGGCTAA 274
DB
267 CTTTATGAGAAAGCTTTAGAGAAATTAATAAAGATGACACAAAACTACTT--- 323
QY
275 ATAGATGATGAAAGCGTAGATGATATTAATTAATCTCCAGAAACGATATCTTACA 334
DB
324 ---CGCTTCAATTAATCAGTGGGTGTATGAAACAGATTATTTAGTATGAGGT 380
QY
335 AGACATGCTCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 394
DB
381 ATGTAGAAAGCGGCAAGGACCGTGGCAGATGATGATGATGATGATGATGATGATG 440
QY
395 ATGTACTGTAGTGTATATATATGATGATGATGATGATGATGATGATGATGATGATG 454
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441 AATGACACATTAAGGTTTCCCAAGGTTGTAAGTGTATGATGATGATGATGATGATG 500
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455 AAGTTAGATCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 514
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501 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 560
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515 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 574
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561 ATTACCAAAATGCTAAGGTAAGTGAATACCAAAAGATGATGATGATGATGATGATG 620
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575 ATATATATTAATTAATTTCTAAGGATATATGATGATGATGATGATGATGATGATG 634
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621 CGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 680
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635 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
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681 CTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 740
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741 TTAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 800
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752 ATCCG-----TACGTAATGATGATGATGATGATGATGATGATGATGATGATG 805
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801 GTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 860
QY
806 GATATCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 865
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861 TACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 920
QY
866 TTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 925
DB
921 AAGCGAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 940
QY
926 AACCAAGCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 945
DB

RESULT 3

US-08-307-499-1/c
; Sequence 1, Application US/08307499

GENERAL INFORMATION:

APPLICANT: Meyer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Sallwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,499
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sallwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14176 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 3852..4226
FEATURE:
NAME/KEY: CDS
LOCATION: 4585..4887
FEATURE:
NAME/KEY: CDS
LOCATION: 5131..5310
FEATURE:
NAME/KEY: CDS
LOCATION: 5760..5912
FEATURE:
NAME/KEY: CDS
LOCATION: 6786..7130
FEATURE:
NAME/KEY: CDS
LOCATION: 10148..10513
US-08-307-499-1

Query Match 12.9%; Score 133.6; DB 1; Length 14176;
Best Local Similarity 49.0%; Pred. No. 3.4e-25;
Matches 451; Conservative 0; Mismatches 454; Indels 15; Gaps 3;

QY 27 TTAGCACAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 86
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QY 994 TTAGCACAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 935
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QY 87 TAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 146
DB TAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 146
QY 934 ATGATATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 875
DB ATGATATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 875
QY 147 CGAAATATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 206
DB CGAAATATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 206
QY 874 GTTAAATATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 815
DB GTTAAATATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 815
QY 207 TTAATATTTCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 266
DB TTAATATTTCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 266
QY 814 TTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 755
DB TTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 755
QY 267 CTTAATGAGAAAGAACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 323
DB CTTAATGAGAAAGAACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 323

Db 754 ATAGAAATGAGTGAAGACCTAGATGAGATTAATAAATCTCCAGAAACGAGTAACTCTTACA 695
Qy 324 ---CGCTTTCATTAATCACTGGGTGTTATGAAACAGAGTATTAATTTGGTAGTTAGGGT 380
Db 694 AGACTATGTCCTTACCAATTGGATGTACTACTAAGACAATCTCAAGTAAATTTGGTT 635
Qy 381 ATGTAGAAACGGCCACGACCGCTGGCCAGATACCATACAGAGATTAAGTTAAAGTTTACGA 440
Db 634 ATGTTACTGTAGGTGATTAATATAGACAGATTCGACCCCAAGAAATAAACGCTTAGTA 575
Qy 441 AAATGACACATTAAGGTTTCCCAAGTTGGATGTTAACTGTAAAAAACACTCTTTGGA 500
Db 574 AAGTTAGATACGACATCTTCCAAAGGTAGAAATGTTAACTGTTAACTCAACACACTGGG 515
Qy 501 AAGATGTAAAAAATCTATCTAGCGGCTTTGAATACATGAGTGTCTATTTAGTATTTAG 560
Db 514 AAGCTGTATGGAACATCTTGATCATGTTAATACATTTCCCTTTACAGCGGATG 455
Qy 561 ATTACCAAAATGCGTTAAAGGTGAATACCAAAAGATACACACCTACAGTAAAGTAA 620
Db 454 ATTATTTAAATTTCTAGGATATATAGATTAAGCCAGTTAAGCCTACTGTACAGTTA 395
Qy 621 CGGATATGAGTGAAGATGATGATACATGACTCTTGATGACAGTAAATTTCACTTTACC 680
Db 394 CAGGAATTTGAAGGAGA---TAACTCATGATGATATGACATTTGATTAATCATTTATC 338
Qy 681 CTCCTGACGTAATTAATTAAGTGAAGACGAACTTTTAAAGGTGAATTAATTAATG 740
Db 337 CGTCGTGCGTGGTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 278
Qy 741 TTAAAGGAATATCTATCCAGATGGGGGAGAAATCCGTTTATGAGCCAGGAGACGAG 800
Db 277 ATCCG-----TACGTAATGAATGCTTCTGATGACGACTATCAACCGGTAACGAC 224
Qy 801 GTTTCCATGGAATATTAATAAAGATTAAGATCAACATTAATTAATTAATTAATTAATG 860
Db 223 GATATCGGACTATTAATGAGATGATGATGATTAATTAATTAATTAATTAATTAATG 164
Qy 861 TACGTACACATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 920
Db 163 TTATGTACCAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 104
Qy 921 AAGCGCAAGTTTAACTGT 940
Db 103 AACCAAGCATTAATGATGT 84

RESULT 4
US-08-307-499-14
Sequence 14, Application US/08307499
Patent No. 5651972
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
TITLE OF INVENTION: Live Vaccine Vector
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,499
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 14176 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 138..1460
FEATURE:
NAME/KEY: CDS
LOCATION: 2456..2659
FEATURE:
NAME/KEY: CDS
LOCATION: 2809..3030
FEATURE:
NAME/KEY: CDS
LOCATION: 3070..3330
FEATURE:
NAME/KEY: CDS
LOCATION: 3356..4180
FEATURE:
NAME/KEY: CDS
LOCATION: 4392..5894
FEATURE:
NAME/KEY: CDS
LOCATION: 6171..6398
FEATURE:
NAME/KEY: CDS
LOCATION: 6447..6875
FEATURE:
NAME/KEY: CDS
LOCATION: 6928..7431
FEATURE:
NAME/KEY: CDS
LOCATION: 7454..7858
FEATURE:
NAME/KEY: CDS
LOCATION: 7895..8155
FEATURE:
NAME/KEY: CDS
LOCATION: 8215..8682
FEATURE:
NAME/KEY: CDS
LOCATION: 8715..9539
FEATURE:
NAME/KEY: CDS
LOCATION: 9562..10272
FEATURE:
NAME/KEY: CDS
LOCATION: 10316..11908
FEATURE:
NAME/KEY: CDS

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NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
US-08-559-896B-1

Query Match 4.1%; Score 42; DB 4; Length 1956;
Best local similarity 49.0%; Pred. No. 0.081;
Matches 141; Conservative 0; Mismatches 145; Indels 2; Gaps 1;

QY 569 AAAAAAGCTAAAGGTGGAATATCCAAAAGATCAACACCTACAGTAAAGTAAAGCGGTAAAT 628
Db 1011 AATATTCACAGATATATACAAAAGAAAATATCAAAATTTAGAACTAGAGAAAATCGATAG 1070
QY 629 GAGTTAGAGATGGTAAACATATGACCTCTGAATGACGTGTAATTCATTTTACCCTCCGAC 688
Db 1071 ACTTTATTAAGACAAATTTAGTATAGATGGATAGAAACAGGTATGAATCCCATGAG 1130
QY 689 GTAATTTCTAAGTGGATAGAAAGCAACCATTTTAAAGGTGAATTAATATGTTAAACGA 748
Db 1131 AATATTTAAGCAGAAATGAAAAGAAAGATATATATATATACATAGAAATATTTAAAAATGAATCTAA 1190
QY 749 AGATACATATCCGAATGGGGAGAAAATCCGATTTATGAGCCAGAGAGACCGATTTCGA 808
Db 1191 CCAAAAAAATAGAAAGAAAATGTATATGTTATATATATACGACACATATATGATAGTAA 1250
QY 809 TGAATATTTAAAAAGATAAAGATGCAAAACATATATGTTAAACAGAT 856
Db 1251 T-TAATATATATATATATATATATATATAGAGATGTAATATATTTAAATATAT 1296

RESULT 9
US-09-004-838-70
; Sequence 70, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmore, Richard W.
; APPLICANT: Shen, Kathy
; TITLE OF INVENTION: Procedures and Materials for
; TITLE OF INVENTION: Confering Pest Resistance in Plants
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-07881005

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 185:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 662 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1073UP
; US-08-998-416-185

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Query Match      3.8%; Score 39.4; DB 4; Length 662;
Best Local Similarity 46.1%; Pred. No. 0.26;
Matches 167; Conservative 0; Mismatches 192; Indels 3; Gaps 1;

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QY 18 TATATATTTTGGACACATTTGACAGTTTGTAACTGATTAATTAATTAATTA 77
DB 602 TATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 543
QY 78 CTGTACGTTAAAGTAATGGGTATACAGTAGAGTATTTACGATCAATTAAC 137
DB 542 TAGATTTTAAAGTATTTCTATTAATTAATTAATTAATTAATTAATTAAT 483
QY 138 AGTTACTAAGCAAAATATCATTAATTAATTAATTAATTAATTAATTAATTA 197
DB 482 AATTAAGGTAGACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 423
QY 198 CTGATGTTTATATTTCTAGAGTCCCAACAGCCAGGTAACAT--TACAATTT 254
DB 422 AAGGTACATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 363
QY 255 ACTTTGGTATCTTAAATGAAGAATCTTTAGAAATTAATTAATTAATTAAT 314
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QY 315 AAACACTCGCTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 374
DB 302 TTAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 243
QY 375 AT 376
DB 242 AT 241

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RESULT 12
US-08-998-416-786/c
; Sequence 786, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippson, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Redischung, Corinne

```

```

; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6239264rtls Corporation
; STREET: 3054 Cornwalis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 786:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1504UP
; US-08-998-416-786

```

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Query Match      3.8%; Score 39; DB 4; Length 711;
Best Local Similarity 45.9%; Pred. No. 0.34;
Matches 172; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

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QY 5 TTCAATGAATTAATTAATTTTATGACAACTTGACAGTTTGTAACTGATTAAT 64
DB 616 TTACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 557
QY 65 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 124
DB 556 GATATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 497
QY 125 CATTAACAAGTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 184
DB 496 GGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 437
QY 185 GTAAATTTTAAAGGCTGATTTGTTAATTTTCTAGAGTCCCAACAGCCAGGTA 244
DB 436 AATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 317
QY 245 ---TCAACTTTAACTTTTGTATTTCTTAATTAATTAATTAATTAATTAAT 301
DB 376 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 317
QY 302 AAGCATGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 361
DB 316 AAAATGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 257
QY 362 TTAATTTGTAATTAAT 376
DB 256 TTAATTTCTAATTAAT 242

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1      RESULT 13
2      US-08-998-416-683/c
3      ; Sequence 683, Application US/08998416
4      ; Patent No. 6239264
5      ; GENERAL INFORMATION:
6      APPLICANT:  Philippson, Peter
7      APPLICANT:  Pohlmann, Rainer
8      APPLICANT:  Steiner, Sabine
9      APPLICANT:  Mohr, Christine
10     APPLICANT:  Wendland, Jurgen
11     APPLICANT:  Knechtle, Philipp
12     APPLICANT:  Reibischung, Corinne
13     TITLE OF INVENTION:  GENOMIC DNA SEQUENCES OF ASHBYA GOSSEYI
14     TITLE OF INVENTION:  AND USES THEREOF
15     NUMBER OF SEQUENCES:  1152
16     CORRESPONDENCE ADDRESS:
17     ADDRESSEE:  No. 6239264artis Corporation
18     STREET:  3054 Cornwallis Road
19     CITY:  Research Triangle Park
20     STATE:  No. 6239264th Carolina
21     COUNTRY:  USA
22     ZIP:  27709
23
24     COMPUTER READABLE FORM:
25     MEDIUM TYPE:  Floppy disk
26     COMPUTER:  IBM PC compatible
27     OPERATING SYSTEM:  PC-DOS/MS-DOS
28     SOFTWARE:  Patentin Release #1.0, Version #1.30
29
30     CURRENT APPLICATION DATA:
31     APPLICATION NUMBER:  US/08/998,416
32     FILING DATE:  24-DEC-1997
33     CLASSIFICATION:  435
34
35     PRIOR APPLICATION DATA:
36     APPLICATION NUMBER:  CH 0016/97
37     FILING DATE:  31-DEC-1996
38     ATTORNEY/AGENT INFORMATION:
39     NAME:  Meigs, J. Timothy
40     REGISTRATION NUMBER:  38,241
41     REFERENCE/DOCKET NUMBER:  PF/5-30306/A/CGC1976
42     TELECOMMUNICATION INFORMATION:
43     TELEPHONE:  919-541-8587
44     TELEFAX:  919-541-8689
45
46     INFORMATION FOR SEQ ID NO:  683:
47     SEQUENCE CHARACTERISTICS:
48     LENGTH:  724 base pairs
49     TYPE:  nucleic acid
50     STRANDEDNESS:  single
51     TOPOLOGY:  linear
52     MOLECULE TYPE:  DNA (genomic)
53     ORIGINAL SOURCE:
54     ORGANISM:  PAG1453RP
55
56     US-08-998-416-683

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Query Match	3.8%	Score 39	DB 4	Length 724
Best Local Similarity	45.9%	Pred. No. 0.34		
Matches	172	Conservative	0	Mismatches 200; Indels 3; Gaps 1
QY	5	TTCAATGAATAGTAAATATATTTTACGCAAAATGTGACAGTTTGAATGCATACTTTA	64	
Db	615	TTACTAATTAATTAATTAATTTAAATATATATAAAAAGATTTAATTAATTTATATCTTTA	556	
QY	65	AAATATATATTTACTGTTACGCTTAAAGATATATGGGTATATGATGAGATATTTACGAT	124	
Db	555	GATATATTAATTTAGATTTAGATTTCTTATATATATATTTAGTTAGTAAATTTTAGTA	496	
QY	125	CATTCACAAGATCGAGTTAGTACGAAATATCATTTAACGAGAACTAGACAGGAAC	184	
Db	495	GGTGTGTAATATCCATTTAAAGGTAGACATATTAATTAAGAAATATATCTACGACTAATATAA	436	
QY	185	GTAATTTTATGGCGTATGTTTAAATTTTCTAGAGTCCGCCACAGCCAGGTACGAT	244	
Db	435	ATAATATTTATGAAGAAGTCAATTTAATATTTATATATATCAATGAAGTAATTTAAATAT	376	
QY	245	---TACAACTTTAACTTTTGGTATTTCTTTAATGAAGAAGAACTTTGAGAAGAAATTAATATA	301	

D _b	375	T T A T T A A A T T A A T A T A T A T A C A C T T A A T A T A T A A A C C T A A P A A N C T A T T A T T A A T	316
O _y	302	A A G A T A G C A C A A A A C T A C T G C T T C A T T A A T A A C T G G G T G T A T G A A A C A G A T T A	361
D _b	315	A A A A A A G C A T A T T A T T A T A T A A A A T T A A A T T A A A C T A T T A T A T A A A A T T C T A A A G	258
O _y	362	T T A T T G G A G T T A T	376
D _b	255	T A A T T C T A T T A T T A T	241

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RESULT 14
US-08-998-416-1036/c
? Sequence 1036 Application US/08998416
? Patent No. 6239264
? GENERAL INFORMATION:
?   APPLICANT: Philippsen, Peter
?   APPLICANT: Pohlmann, Rainer
?   APPLICANT: Steiner, Sabine
?   APPLICANT: Mohr, Christine
?   APPLICANT: Wendland, Jürgen
?   APPLICANT: Knechtle, Philipp
?   TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBVA GOSYPHYLLUM
?   TITLE OF INVENTION: AND USUS THERIOF
?   NUMBER OF SEQUENCES: 1152
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: No. 6239264artis Corporation
? STREET: 3054 Cornwallis Road
? CITY: Research Triangle Park
? STATE: No. 6239264th Carolina
? COUNTRY: USA
? ZIP: 27709
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/998,416
? FILING DATE: 24-DEC-1997
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: CH 0016/97
? FILING DATE: 31-DEC-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Meigs, J. Timothy
? REGISTRATION NUMBER: 38,241
? REFERENCE/DOCKET NUMBER: PF/5-30306/A/GC1976
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 919-541-8587
? TELEFAX: 919-541-8689
? INFORMATION FOR SEQ ID NO: 1036:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 732 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? ORIGINAL SOURCE:
? ORGANISM: PAG16330P
? US-08-998-416-1036

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Query Match	3.8%;	Score 39;	DB 4;	Length 732;
Best Local Similarity	45.9%;	Pred. No. 0.34;		
Matches 172;	Conservative 0;	Mismatches 200;	Indels 3;	Gaps 1

QY	5	TTCATGAAATAGGTATATATTATTAGCACATTTGACAGCTTTGACTGCATACCTTA	64
Db	615	TTCCTATTTATATATATTATATATATATATATATATATATATATATATATATATCTTAA	556
	65	AAATATATATATACCTGTTACGTTAAAGATATGCGTTATACGATGAGATATTTACGAT	124

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 20:15:21 ; Search time 1497 Seconds
(without alignments)
1186.462 Million cell updates/sec

Title: US-09-976-605-5

Perfect score: 1034
Sequence: 1 aagctcatgataaagtaaa.....agaagacgaacccctcgag 1034

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	6.0	1161	BE421968	BE421968 HMM017CF
2	59.8	5.8	1101	CNS0039G	AL063921 Drosophila
3	59.8	5.8	1101	CNS003BD	AL064091 Drosophila
4	57.4	5.6	1101	CNS0182P	AL108811 Drosophila
5	55.8	5.4	938	CNS006TJ	AL065906 Drosophila
6	53.2	5.1	843	CNS00CST	AL053666 Drosophila

7	53.2	5.1	1225	17	CNS0161D	AL106171 Drosophila
8	52.8	5.1	974	17	CNS0017T	AL075432 Drosophila
9	52	5.0	997	17	CNS005RE	AL060767 Drosophila
10	51.8	5.0	538	9	AU053236	AU053236 AU053236
11	51.8	5.0	928	17	CNS00DKY	AL071865 Drosophila
12	51.8	5.0	928	17	CNS00EVL	AL069706 Drosophila
13	51.2	5.0	581	17	CNS01UP2	AL168128 Tetradon
14	50.8	4.9	385	14	BO596570	BO596570 Pterodon
15	50.6	4.9	1101	17	CNS0006T	AL068204 Drosophila
16	50.2	4.9	928	17	CNS0102F	AL068433 Drosophila
17	49.6	4.8	1101	17	CNS00E07	AL069440 Drosophila
18	49.4	4.8	1101	17	CNS0067Y	AL063308 Drosophila
19	49.2	4.8	734	17	CNS010MP	AL069163 Drosophila
20	49	4.7	909	17	CNS012AT	AL101327 Drosophila
21	49	4.7	1101	17	CNS0039G	AL063921 Drosophila
22	49	4.7	1101	17	CNS0039R	AL063932 Drosophila
23	48.8	4.7	629	13	BU422197	BU422197 BU422197
24	48.6	4.7	928	17	CNS00DKY	AL071865 Drosophila
25	48.6	4.7	987	17	CNS014PQ	AL104456 Drosophila
26	48.2	4.7	888	17	CNS007VQ	AL050896 Drosophila
27	48.2	4.7	1031	17	CNS00CE2	AL059199 Drosophila
28	48.2	4.7	1101	17	CNS008X3	AL052544 Drosophila
29	48	4.6	639	17	CNS017GD	AL108367 Drosophila
30	48	4.6	878	17	CNS0187R	AL108993 Drosophila
31	47.8	4.6	1225	17	CNS0161D	AL106171 Drosophila
32	47.8	4.6	500	9	AU087771	AU087771 AU087771
33	47.8	4.6	1101	17	CNS000B8	AL063632 Drosophila
34	47.6	4.6	877	17	AZ531291	AZ531291 ENTBQ34R
35	47.6	4.6	879	17	CNS01JRG	AZ531291 Anopheles
36	47.6	4.6	908	17	AZ548467	AZ548467 ENTEFJ2TF
37	47.6	4.6	912	17	AZ551092	AZ551092 ENTEFJ2TF
38	47.6	4.6	1101	17	CNS00CYH	AL060100 Drosophila
39	47.6	4.6	1101	17	CNS00EPO	AL069493 Drosophila
40	47.6	4.6	1184	13	BM545225	BM545225 AGENCOURT
41	47.4	4.6	945	17	CNS04DOK	AL285149 Tetradon
42	47.4	4.6	1092	17	CNS020K7	AL175636 Tetradon
43	47.4	4.6	1200	17	CNS016EL	AL106647 Drosophila
44	47.2	4.6	961	17	CNS008H1	AL051882 Drosophila
45	47.2	4.6	1101	17	CNS000D1	AL065414 Drosophila

ALIGNMENTS

RESULT 1
LOCUS BE421968
DEFINITION HMM017CF.08r ITFC HMM Barley leaf library Hordeum vulgare cDNA
ACCESSION BE421968
VERSION BE421968.1 GI:9419811
KEYWORDS EST.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.

REFERENCE
AUTHORS Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemelin, J.M., Jia, J., Joudrier, P., Langridge, P., Izzo, G.R., Lin, J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M., and Wenzel, G.
International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
Published (2000)
Contact: Wenzel G
TU Munchen, Lehrstuhl fur Pflanzenbau und Pflanzenzuchtung
Am Hochanger 2, D-85350 Freising-Weihenstephan GERMANY
Fax: 49 08161 71 5173
Email: wenzel@umw.phz.agrar.tu-muenchen.de
International Triticeae EST Cooperative (ITEC)

JOURNAL
COMMENT

Db	618	DMRTADRDNRNAATWTDIARKADSDMKASAMRBDRAPAAARDSRWTTKGTATTAAW	559
QY	800	GGTTTTCCAGGCAATATTAATAAAGATAGATCAACACATATAGTTTAAACAGTTTA	859
Db	558	TTTAAAGAAAMAMAMAMATTAATTAATTTTWTWTWTWTWTWTWTWTAAAMAAWTTTAA	499
QY	860	GTACGTACAACATCAAAAATGAGTAGTCACACTAGTGTGTTTCCATGACACTTAA	919
Db	498	WTAAAAAAMAAAAAMAAATTTTTTTTTTWTAAATAAMWTATWTWTWTWTWTAAATTTTT	439
QY	920	GAAGCGCAGGTTTAACTGTGTCGAA	946
Db	438	TWTWTMAATTAATTTTWTWTAAAA	412

RESULT 3	CNS003BD	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
	CNS003BD	1101 bp	DNA	linear	GSS 03-JUN-1999			
	Drosophila melanogaster	genome survey sequence	TE13 end of BAC #	BACR08K08 of RPe1-38 library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
	AL064091							
	AL064091.1	GI:4941847						
	GSS.							
	Drosophila melanogaster.							
	Drosophila melanogaster							
	Drosophila melanogaster							

REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
1 (bases 1 to 1101)	
Genoscope.	
Direct Submission	
Submitted (02-JUN-1999)	Genoscope - Centre National de Séquençage :

FEATURES	COMMENT
	<p>determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org/The BDGP Drosophila melanogaster BAC library was prepared by Kazuhiro Onoeawa and Aaron Mammoser in Pletier de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPcl-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.</p>

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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR08K08"
/clone_1b="RPC1-98"
/notes="end : Tef3"
395 a 120 c 103 g 334 t 149 others
BASE COUNT
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[illegible]

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Db	647	TAATTTTTTAAATTTTTTATTATTANNMAAMATTTTTAAAAAAAAAAAAAAAAAAAAATATAA	706
QY	419	ACAGAGATTAAGAGTTTACGAAATGACATTAAGGTTTCCAGAGTTGCAGTGA	478
Db	707	AAAAAAAAATTATTAAMTWTATTAATATATATTTTAAATAATATTTTAAAAAAAAAAATATWT	766
QY	479	ACTGTAAAAAACACTCTTTGGAAAGATGTAAAAACCTATCTAGCGCTTTTGAAATACATG	538
Db	767	ATTATATATTTAAAAATATATATATTTATATATATNMNATATWTTTTAAATTWTATATWT	826
QY	539	GGATGTTGATAGCATTTTGTAGATTACCAAAAAAATGGCTAAAGGTGAAATGCCAAAGAT	598
Db	827	--AATWTATTTTAAAMATTTTAAATTAATAAAAAAAAAAAAAATAAATAATATATWTATWTAT	884
QY	599	ACAACACCCTACAGTGAAGATGAACGGGTATGATGTAGAAAGATGTGAACATGACCTGTGA	658
Db	885	AMTWTTTMAATTAATTAATTAATTAAMMAAAAAAAAAAATTAAMTATTAATAATTAATTTWT	944
QY	659	TGCGAGTGAATTCATTTTACCCCTCCAGCTAAATTACTAAGTGATGAAGAACCGAACAT	718
Db	945	YTAAAAAAMWTMTTMAWMAAATAATTTTATATWTATTAATTAATTAATMAAAAAAAAAAAAAATAA	1004
QY	719	TTTAAGGTGAATATAAAT 739	
Db	1005	AATTAATAATTNMAAMWATATAAM 1025	

RESOLUTION	CNS0182P	1101 bp	DNA	linear	GSS 26-JUL-1999
LOCUS	CNS0182P				
DEFINITION	Drosophila melanogaster genome survey sequence Sp6 end of BAC BACN37D10 of drosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL108811				
VERSION	AL108811.1	GI:5629115			
KEYWORDS	GSS.				
SOURCE	Drosophila melanogaster.				
ORGANISM	Drosophila melanogaster				

REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de séquençage :

COMMENT

determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaut at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES	
source	location/Qualifiers
	1. .1101
	/organism="Drosophila melanogaster"
	/db_xref="taxon:7227"
	/clone="BACN37D10"
	/clone_1lb="DrosBAC"
	/plasmid="pBelosBAC11"
	/note="end : Sp6"
BASE COUNT	274 a 268 c 128 g 73 t 358 others
ORIGIN	

Query Match	5.68;	Score 57.4;	DB 17;	Length 1101;
Best Local Similarity	19.3%;	Pred. No. 0.071;		
Matches	90;	Conservative 184;	Mismatches 193;	Indels 0;
				Gaps 0

[illegible]

RESULT 5
CNS006TJ/c

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

CNS006TJ 938 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BAC1411 of RpCl-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL065906
AL065906.1 GI:4944874
GSS.
Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephyridioidae; Drosophilidae; Drosophila.
1 (bases 1 to 938)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazuhiro Osoegawa and
Aaron Mammotser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RpCl-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC resource Center can be
found at http://bacpac.med.buffalo.edu/Drosophila_bac.htm.

FEATURES	Location/Qualifiers
source	1..938
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	/db_xref="taxon:7227"
	/clone="BACR14J11"
	/clone_1lb="RPCT-98"

BASE COUNT	86 a	98 c	85 g	334 t	335 others
ORIGIN					

Query Match 5.48; Score 55.8; DB 17; Length 938;
Best Local Similarity 22.48; Pred. No. 0.15;
Matches 103; Conservative 149; Mismatches 208; Indels 0; Gaps 0

[illegible]

CNSN00CS1/C					
LOCUS	CNSN00CS1	843 bp	DNA	linear	GSS 04-JUN-1999
DEFINITION	<i>Drosophila melanogaster</i> genome survey sequence TE73 end of BAC # BACC26H19 of RPCI-98 library from <i>Drosophila melanogaster</i> (fruit fly), genomic survey sequence.				
ACCESSION	AL059666				
VERSION	AL059666.1	GI:	4947129		
KEYWORDS	GSS.				
SOURCE	<i>Drosophila melanogaster</i> .				
ORGANISM	<i>Drosophila melanogaster</i> . <i>Eukaryota</i> ; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachytera; Muscomorpha; Ephyridroidea; Drosophilidae; <i>Drosophila</i> .				
REFERENCE	1 (bases 1 to 843) Genoscope.				
AUTHORS	Direct Submission				
TITLE	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage ; BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr				
JOURNAL	Web : www.genoscope.cns.fr)				
COMMENT	determination of this BAC-end sequence was carried out as part of a				

melanogaster BAC library was prepared by Kazuhiro Osoegawa and Aaron Mermaster in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPII-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers

1. 843
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR26H19"
/clone_11b="RPC1-98"
/note="end : TET3"

BASE COUNT 131 a 102 c 259 g 141 t 210 others

Query Match 5.1%; Score 53.2; DB 17; Length 843;
Best Local Similarity 34.4%; Pred. No. 0.51;
Matches 101; Conservative 58; Mismatches 135; Indels 0; Gaps 0;

QY 8 ATGATAGTAAATATATATAGACAAATTTAGCAGTTTACATGATTAACATTA 67
DB 783 ATATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 724
QY 68 TATAATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 127
DB 723 TAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 664
QY 128 TACAACGATCAGTTAGTACGAAATATCATATTAACGACGAACTAGACGAA 187
DB 663 TTAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 604
QY 188 AATTTTGGCGTATGTTTATTTATTTCTAGAGTCCCGACAGCCGATGATGAT 247
DB 603 AAAAAAATAAT 544
QY 248 AACTTAATCTTGTATCTTATATGAAAGAACTTAGAAGAAATTAATAA 301
DB 543 MAATTAATAAT 490

RESULT 7
LOCUS CNS0161D 1225 bp DNA linear GSS 26-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence Sp6 end of BAC
BACN15C18 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION AL106171.1 GI:5620504
VERSION AL106171.1
KEYWORDS GSS.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.

REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1225)
Genoscope.
Direct Submission
Submitted (23-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (BDGP) -
<http://www.edgp.ebi.ac.uk> - . This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billand at CERN (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES

Location/Qualifiers

1. 1225
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN15C18"
/clone_11b="DrosBAC"
/plasmid="pBelobAC11"

BASE COUNT 266 a 128 c 38 g 368 t 425 others
ORIGIN

Query Match 5.1%; Score 53.2; DB 17; Length 1225;
Best Local Similarity 32.6%; Pred. No. 0.52;
Matches 103; Conservative 65; Mismatches 148; Indels 0; Gaps 0;

QY 1 AAGCTTCATGAAAT 60
DB 900 WATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 959
QY 61 TTTAATAAT 120
DB 960 WTTTAAAT 1019
QY 121 CGATCATTTACAGATCAGTTAGTACGAAATATCATATTAACGACGAACTG 180
DB 1020 AAAAAAATAAT 1079
QY 181 AAACGTAATTTTATGAGCTGATGTTTATATTTCTAGAGTCCCGACAGCGAT 240
DB 1080 WATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1139
QY 241 CGATTTACACTTTTATCTTTGTTATTTCTTAATGAAAGAACTTAGAAGAA 300
DB 1140 AATTTTAAAT 1199
QY 301 AAACGATGACCAAAA 316
DB 1200 AAAAAATMAAATAATA 1215

RESULT 8
LOCUS CNS001TT 974 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR37D06 of RPC1-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION AL075432
VERSION AL075432.1 GI:4954990
KEYWORDS GSS.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.

REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 974)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : <http://www.genoscope.cns.fr>)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Oosawa and
Aaron Mammosser in Pter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPC1-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain v2; cn bw sp. the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

1. 974
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR37D06"

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QY 478 AACGTAAAAAACACCTCTTTGGAAAGATGTAAAACTATCTAGCGGCTTTCAATACAT 537
|| : || ||| | : : || | : : | | || | :
Db 549 AAAMATATKAAATTTTTRRRRRRACGATTTTBDTRAKAAAAAAAATATTTGAAAAARG 608

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 20:20:31 ; Search time 186 Seconds

(without alignments)
8049.972 Million cell updates/sec

Title: US-09-976-605-5

Perfect score: 1034
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Scoring table: IDENTITY_NTCT
Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 72403093 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1034	100.0	1034	US-09-976-605-5	Sequence 5, Appl1
2	986.6	95.4	1017	US-09-976-605-7	Sequence 7, Appl1
3	571.6	55.3	1183	US-09-976-605-3	Sequence 3, Appl1
4	133.6	12.9	1023	US-09-976-605-8	Sequence 9, Appl1
5	44.6	4.3	7195	US-10-239-676-30	Sequence 30, Appl1
6	43	4.2	519	US-09-878-574-4292	Sequence 4292, Ap
7	42	4.1	1956	US-09-351-794A-1	Sequence 1, Appl1
8	42	4.1	402850	US-09-844-653-5	Sequence 5, Appl1
9	41.6	4.0	563	US-09-864-761-13293	Sequence 13293, A
10	41	4.0	2000	US-09-938-842A-3532	Sequence 3532, App
11	40.2	3.9	6204	US-10-239-676-190	Sequence 190, App
12	40	3.9	335913	US-09-754-853A-2	Sequence 2, Appl1
13	40	3.9	335913	US-09-754-853A-3	Sequence 3, Appl1
14	39.8	3.8	640681	US-09-790-988-1	Sequence 1, Appl1
15	39.6	3.8	640681	US-09-790-988-1	Sequence 1, Appl1
16	39.2	3.8	28897	US-09-764-877-3897	Sequence 3897, Ap
17	39	3.8	6022	US-10-239-676-80	Sequence 80, Appl1
18	39	3.8	9539	US-10-239-676-51	Sequence 51, Appl1
19	38.8	3.8	465	US-09-918-995-13214	Sequence 13214, A

C	20	38.8	3.8	7906	9	US-10-239-676-97	Sequence 97, Appl1
C	21	38.6	3.7	1503841	9	US-09-946-807-1	Sequence 1, Appl1
C	22	38.6	3.7	1503841	10	US-09-795-668-1	Sequence 1, Appl1
C	23	38.6	3.7	1503841	10	US-09-795-668-1	Sequence 1, Appl1
C	24	38.4	3.7	12465	9	US-10-239-676-31	Sequence 31, Appl1
C	25	38	3.7	3825	12	US-10-051-952-8	Sequence 8, Appl1
C	26	37.8	3.7	2244	7	US-08-781-986A-270	Sequence 270, App
C	27	37.8	3.7	8895	9	US-10-091-438-250	Sequence 250, App
C	28	37.8	3.7	8895	9	US-10-091-438-250	Sequence 250, App
C	29	37.8	3.7	8895	10	US-10-091-438-256	Sequence 887, App
C	30	37.8	3.7	8895	10	US-09-764-883-887	Sequence 937, App
C	31	37.8	3.7	8895	10	US-09-764-883-887	Sequence 246, App
C	32	37.8	3.7	9656	9	US-10-091-438-246	Sequence 886, App
C	33	37.8	3.7	9656	9	US-10-091-438-246	Sequence 933, App
C	34	37.8	3.7	9656	10	US-09-764-883-886	Sequence 255, App
C	35	37.8	3.7	32204	9	US-09-764-883-933	Sequence 886, App
C	36	37.8	3.7	32204	9	US-10-072-349-327	Sequence 517, App
C	37	37.8	3.7	32204	10	US-09-764-885-327	Sequence 327, App
C	38	37.6	3.6	2530	10	US-09-813-320-3	Sequence 3, Appl1
C	39	37.6	3.6	5979	9	US-10-239-676-13	Sequence 2332, Ap
C	40	37.6	3.6	5979	9	US-10-239-676-13	Sequence 18, Appl1
C	41	37.4	3.6	5935	9	US-09-991-936-1334	Sequence 1334, App
C	42	37.2	3.6	550	9	US-09-938-842A-3739	Sequence 3739, App
C	43	37.2	3.6	4285	9	US-10-104-580-1	Sequence 1, Appl1
C	44	37.2	3.6	281	10	US-09-864-761-24730	Sequence 24730, A
C	45	36.8	3.6				

ALIGNMENTS

RESULT 1
US-09-976-605-5
; Sequence 5, Application US/09976605
; Patent No. US20020102535A1
GENERAL INFORMATION:
; APPLICANT: MCFADEN, GRANT
; APPLICANT: ESSANI, KARIM
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES
; FILE REFERENCE: 50082/015002
; CURRENT APPLICATION NUMBER: US/09/976, 605
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/239, 354
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1034
; TYPE: DNA
; ORGANISM: Tanapox virus
US-09-976-605-5

Query Match	100.0%	Score 1034;	DB 10;	Length 1034;
Best Local Similarity	100.0%	Pred. No. 7, 7e-222;		
Matches 1034;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1	AAGCTTCATGATAGTTAATATATTATTAGACATTTGTACGATGACATAAC	60	
DB	1	AAGCTTCATGATAGTTAATATATTATTAGACATTTGTACGATGACATAAC	60	
OY	61	TTTAAATATATATATCTGTACGTTAAAGATATGAGTTATACGATGATATTTA	120	
DB	61	TTTAAATATATATATCTGTACGTTAAAGATATGAGTTATACGATGATATTTA	120	
OY	121	CGATCATTAACAGCATGATAGTATAGCAAAATATCATATACACGAAACTAGACCG	180	
DB	121	CGATCATTAACAGCATGATAGTATAGCAAAATATCATATACACGAAACTAGACCG	180	
OY	181	AAAGCTAAATTTTGGGCTATGTTTATATTTTACAGAGTCCACACGCGCAGGTAA	240	
DB	181	AAAGCTAAATTTTGGGCTATGTTTATATTTTACAGAGTCCACACGCGCAGGTAA	240	


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QY 241 CGATTACACCTTTTACCTTTGGTATTCCTTTAATGAAGAACTTTAGAGAAATTAATTA 300
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DB 241 CGATTACACCTTTTACCTTTGGTATTCCTTTAATGAAGAACTTTAGAGAAATTAATTA 300
QY 301 AAACGATGACACAAAACCTACTCTGCTTCATTAACTAGTGGTGTATGAAACAGAT 360
    |||
DB 301 AAACGATGACACAAAACCTACTCTGCTTCATTAACTAGTGGTGTATGAAACAGAT 360
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DB 361 AATTATTTGGTATGATGGGTATGTAAGAAAGCCAGGACCGCTGGCCAGTACCAT 420
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DB 421 AGGAGATTAAGAGTTTACGAAATGACACATTAAGTTTCCCAAGTTGGATGTTAAC 480
QY 481 TGTAAAAACACTCTTTGGAAAGATGTAAAACTTATCTAGCCGTTTGTAAATGAGG 540
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DB 481 TGTAAAAACACTCTTTGGAAAGATGTAAAACTTATCTAGCCGTTTGTAAATGAGG 540
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DB 661 CAGTGTAAATTCATTTTACCTCCCTGACGTAACTTCAAGTGAAGTGAAGACGAACTTT 720
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    |||
DB 721 TAAAGGTGAATTAATATATGTTAACGAAAGATTAATCAAGATGGGGGAGAAATCCGA 780
QY 781 TTATGACGACGAGAGCCAGGTTTCCATGCAATTTAAAAAGTAAAGTGAAGTGAAGAC 840
    |||
DB 781 TTATGACGACGAGAGCCAGGTTTCCATGCAATTTAAAAAGTAAAGTGAAGTGAAGAC 840
QY 841 AATATAGTTTACAGATTTAGTACGTACAAATCAAAATGAGTACCACTAGTATGCT 900
    |||
DB 841 AATATAGTTTACAGATTTAGTACGTACAAATCAAAATGAGTACCACTAGTATGCT 900
QY 901 TGTATTCATGACACTTTAGAAAGCCAAAGTTTAACTGTTCTGAGATGCAATGAGA 960
    |||
DB 901 TGTATTCATGACACTTTAGAAAGCCAAAGTTTAACTGTTCTGAGATGCAATGAGA 960
QY 961 GGTATGACGACGACCTATATAGAAAAACAGAGAGAGAGTGAAGAGATGAAGAGA 1020
    |||
DB 961 GGTATGACGACGACCTATATAGAAAAACAGAGAGAGAGTGAAGAGATGAAGAGA 1020
QY 1021 CGGAAACCTCGAG 1034
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DB 1021 CGGAAACCTCGAG 1034

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RESULT 2
US-09-976-605-7
; Sequence 7, Application US/09976605
; Patent No. US20020102535A1
; GENERAL INFORMATION:
; APPLICANT: MCPADEN, GRANT
; APPLICANT: ESSANI, KARIM
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES
; FILE REFERENCE: 50082/015002
; CURRENT APPLICATION NUMBER: US/09/976,605
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/239,354
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 7
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Yaba-like disease virus
US-09-976-605-7
Query Match          95.4%; Score 986.6; DB 10; Length 1017;
Best Local Similarity 98.1%; Pred. No. 3.1e-211;
Matches 998; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 8 ATGATATAGTATATATTTAGCAAAATTTAGCAAGTTTGTAACTTAATTA 67
    |||
DB 1 ATGATATAGTATATATTTAGCAAAATTTAGCAAGTTTGTAACTTAATTA 60
QY 68 TATATATATCTGTACGTTAAAGATTAATGGTATTAAGATGATATTTACGATCAT 127
    |||
DB 61 TATATATATCTGTACGTTAAAGATTAATGGTATTAAGATGATATTTACGATCAT 120
QY 128 TACAGAGTACGTTAGTACGAAATATCATATTAACACGAAACTAGACGGAACGTA 187
    |||
DB 121 TACAGAGTACGTTAGTACGAAATATCATATTAACACGAAACTAGACGGAACGTA 180
QY 188 AATTTAGGCGTATGTTGTTATATTTCTAGAGTCCCAACGCGAGTAAAGTATAC 247
    |||
DB 181 AATTTAGGCGTATGTTGTTATATTTCTAGAGTCCCAACGCGAGTAAAGTATAC 240
QY 248 AACTTTACTTTGGTATTCCTTAATGAAGAACTTTAGAGAAATTAATTAACGAT 307
    |||
DB 241 AACTTTACTTTGGTATTCCTTAATGAAGAACTTTAGAGAAATTAATTAACGAT 300
QY 308 AGCAAAAACTACTTCGCTTTCATTAATCAACGCGGTTAGAAACAGATTAATTT 367
    |||
DB 301 AGCAAAAACTACTTCGCTTTCATTAATCAACGCGGTTAGAAACAGATTAATTT 360
QY 368 GGTATGATGGGTATGTAAGAAAGCCCAACGACGCTTGGCCAGATACAGAGAT 427
    |||
DB 361 GGTATGATGGGTATGTAAGAAAGCCCAACGACGCGTGGCCAGATACAGAGAT 420
QY 428 AAAAGGTTTACGAAATGACACATTAAGGTTTCCCAAGGTTGGAATGTTAACTGTA 487
    |||
DB 421 AAAAGGTTTACGAAATGACACATTAAGGTTTCCCAAGGTTGGAATGTTAACTGTA 480
QY 488 AACCTCTTTGGAAGATGTAAGAACTTATCTAGGCGGTTTGAATACATGGATGTCA 547
    |||
DB 481 AACCTCTTTGGAAGATGTAAGAACTTATCTAGGCGGTTTGAATACATGGATGTCA 540
QY 548 TTACCTATTTAGATTACCAAAAAATGCTTAAAGTGAATACCAAAAGTACACACT 607
    |||
DB 541 TTACCTATTTAGATTACCAAAAAATGCTTAAAGTGAATACCAAAAGTACACACT 600
QY 608 ACACTGAAGTAAGGCTATGATGTTAGAAAGTGTAACTGACTCTTGAATGACAGTGA 667
    |||
DB 601 ACACTGAAGTAAGGCTATGATGTTAGAAAGTGTAACTGACTCTTGAATGACAGTGA 660
QY 668 AATTCATTTTACCCTCTGACGTAAATTAATGATGTAAGAAAGCAAACTTTTAAAGT 727
    |||
DB 661 AATTCATTTTACCCTCTGACGTAAATTAATGATGTAAGAAAGCAAACTTTTAAAGT 720
QY 728 GAATATTAATATGTTAACGGAAGTACTATCCAGAAATGGGGGAGAAATCCGATTAG 787
    |||
DB 721 GAATATTAATATGTTAACGGAAGTACTATCCAGAAATGGGGGAGAAATCCGATTAG 780
QY 788 CCAGAGAGCGAGGTTTCCATGATGATTAATTAATTAATTAATGCAAAACATATATG 847
    |||
DB 781 CCAGAGAGCGAGGTTTCCATGATGATTAATTAATTAATTAATGCAAAATATATATG 840
QY 848 TTAACAGATTTAGTACGTACCAACATCAAAATGATGATGATGATGATGATGATG 907
    |||
DB 841 TTAACAGATTTAGTACGTACCAACATCAAAATGATGATGATGATGATGATGATG 900
QY 908 CATGACACTTTAGAAAGCGCAAGTTTAACTGTTCTGAAGATGCAATGAGAGCTATAC 967
    |||
DB 901 CATGACACTTTAGAAAGCGCAAGTTTAACTGTTCTGAAGATGCAATGAGAGCTATAC 960

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QY	27	TTTGCCAACTTGTGACAGTTTGTAACTGGATACCTTTAAATATATTAATTAAGTCTTACGT	86
Db	35	TTACACCATATGTAGTACTGCTTCCGCACTTTTGTATACAAATTTATCATTAATCTTACAG	94
QY	87	TAAAGATTAATGGTTATACGATGAGATTTTATACGATCATTAACAAGTACGTAGTAA	144
Db	95	ATGATTAATCATCGATATGACTTCGAAGTACCGGATTTATTAATGATTTACTAAATAAAC	153
QY	147	CGAAATATCATATTAACACGAAACTAGACACGGAACGTAAATTTTAGGGCTGATTTGT	206
Db	155	GTTTAAATTAATATGACGAGACGGAACACCGAATTTAAGAAATGAACCAACAACATGCT	214
QY	207	TTAATATTTTCTGGAGTCCGCCACAGCCACGATTAACGATTTACAACTTTTGGTAATT	266
Db	215	TTAATGAGACTAAGTTTGAATTTTATTCGGAATAAATAATTAATTTATGTTGGCGCTAA	274

Query Match	4.1%: Score 42; DB 10; Length 1956;
Best Local Similarity	49.0%: Freq. No. 10;
Matches 141; Conservative 0; Mismatches 145; Indels 2; Gaps 1;	
QY 569 AAAATGGCTAAAGGTGAATATCCAAAGATGCAACACCTACAGTGAAGTAAACGGGTAT	628
Db 1011 AATTTTACAGATTTACAAAAGAAAATATCAAAATTTAGAACAGAAAATCGATAG	1070
QY 629 GAGTTAGAAAGTGTAAACATGACCTCTGAATGACAGCTGTAATTCATTTTACCTCTGAC	688
Db 1071 ACCTTATTAAGAAACAATTAGATACAAATGGATAGAAACAGATGTGAATCCCATGAG	1130
QY 689 GTAAATCTAAGTGATAGAAAGCGAACATTTTAAAGGTGAATTAATATGTTAAACGA	748
Db 1131 AAAATTTAGCGAAGAAATGAAAAGATTAATATTATCATGGAATATTTAAAAATGATCTAA	1190
QY 749 AGATACATATCCAGATGGGGGAAATCCGATATGAGCCGAGAGAGCCAGTTTCCA	808
Db 1191 CCAAAAATAATAGAAAACAAAATGTAATGTATTATATACGACAAATATGATAGTAA	1250
QY 809 TGCATATTTAAAAAGATTAAGATGCAACACATATAGTTTAACAGAT	856
Db 1251 T--AAATATATATAATAATAATAAATAGAGATGGAATATTTAAATATAT	1296

RESULT 8
US-09-844-653-5/c
; Sequence 5, Application US/09844653

	Query Match	4.18;	Score 42;	DB 9;	Length 402850;
	Best Local Similarity	51.68;	Pred. No. 1.e+02;		
	Matches 96;	Conservative 0;	Mismatches 90;	Indels 0;	Gaps 0;
QY	31 CACAAATTGACGAGTTTGTAACGCATTAACCTTTAAATATATATATACGTGTACGTTAA	90			
Db	160962 CAGTATGTTCCAGAGTTCAAGAAGGTCCTTTACACCATATATATATGTTTAGCAAC	1609030			
QY	91 AGATATAGGCTTATACGATGAGATATTTTACGATCATTACAAGCATGAGTTAGTAAGAA	150			
Db	160902 TGTGTGAAGATAGAGGAGGAGCGTTTTACAGATATATATATATCTGTGTCGCA	160843			
QY	151 AATATCATATACCAAGAACTAGACACAGGAAGTAATTTTGGGCTATATGGTTTAA	210			
Db	160842 TTAAGCTTTTAAAGAAAAAGACAAAGGGGACTTTATTTTCTTATATATAGTTCA	160783			
QY	211 TATTTTC 216				
Db	160782 AATCTC 160777				

RESULT 9
US-09-864-761-13293
Sequence 13293, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Aecm1ca-x-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 PRIOR FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 13293
 LENGTH: 563
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO ACO12404.4
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
 US-09-864-761-13293

Query Match 4.0%; Score 41.6; DB 10; Length 563;
 Best Local Similarity 51.0%; Pred. No. 7.4;
 Matches 98; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 835 AACACATATAGTTTACAGATTAGTACGTACACATATAAAGAGTAGCACTAGT 894
 DB 112 AATTAATATATCTTTAAATGTAAAGATGAAATAATGTAAAGATTAATTAACAGT 171
 QY 895 ATGTGTGTTTCCATGACACCTTACAGCGCAAGTTTACTTGTCTGAGAGATGCA 954
 DB 172 TCCACACGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 231
 QY 955 TGGAGAGCTATACGACCTATATAGAAAACAGAAAGAAAGAAAGTGAAGAGATGA 1014
 DB 232 GGAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 291
 QY 1015 AGAAGACGAAA 1026

DB 292 AGAAGAAAGAAAGAA 303

RESULT 10
 US-09-938-842A-3532
 ; Sequence 3532, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Krebs, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SCRIP1300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 3532
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-3532

Query Match 4.0%; Score 41; DB 9; Length 2000;
 Best Local Similarity 45.7%; Pred. No. 18;
 Matches 143; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 55 CATACCTTAAATATATATATCTGTACGTAAAGAAATAGGCTTATACATGAGT 114
 DB 362 CATAGAAATGAAACAAATGATATGTAATGTAACCAAAAGGTGAACATTAATTTTA 421
 QY 115 ATTATGACATTTACAAAGATCAGTATGTAAGAAATATACCAAGCAAGAACTAG 174
 DB 422 ACATTAAGATTTACAAATTAATCATTTATGATTTGTTATTAATTCATTAATAAT 481
 QY 175 ACACGGAAGCTAAATTTAGGCGTGAATGTTTAAATTTCTAGAGAGTCCACAGCC 234
 DB 482 AAGTCTGTATGATGATTTAAATTAATTAATTAATTAATTAATTAATTAATTT 541
 QY 235 AGTAAAGATTTACAACTTTTACCTTGTATGTTTATGTAAGAAAGAACTTACAGAAAT 294
 DB 542 ATTTATAGTAAATTTAAATTTATTTACAAATTTAAATTTTACCTTTAAACAT 601
 QY 295 TAAATAAAGATGACAAATACTCTGCTTCAATTAATGATGAGTGGTGTATGAAC 354
 DB 602 TTATTTATCAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 661
 QY 355 AGATTTATTTT 367
 DB 662 AGTATATATATAT 674

RESULT 11
 US-10-239-676-190/c
 ; Sequence 190, Application US/10239676
 ; Publication No. US20030082609A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OLEK, Alexander
 ; APPLICANT: PIPENBROCK, Christian
 ; APPLICANT: BERLIN, Kurt
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
 ; FILE REFERENCE: 5013.1003
 ; CURRENT APPLICATION NUMBER: US/10/239,676
 ; CURRENT FILING DATE: 2002-09-24
 ; PRIOR APPLICATION NUMBER: PCT/EP01/03968

DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
PRIOR FILING DATE: 2001-04-06
2000-04-06
2000-04-07
2000-06-30
2000-09-01
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 190
LENGTH: 6204
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-239-676-190

Query Match 3.9%; Score 40.2; DB 9; Length 6204;
Best Local Similarity 50.8%; Pred. No. 44;
Matches 96; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 428 AAAAGTTACGAAATGACATGAAGGTTTCCCAAGTTGGAAAGTTAACTGTAATA 487
DB 2352 AAAACATATATTAATTCATTAATAATAATATATCAAAATTAACATAATATAA 2293
QY 488 AACACTCTTGGAAAGATGTAATACTATCTAGCGGTTTGAATCATGGATGTCA 547
DB 2292 TAAATCTCTTTTAAATTTTATCTTAACTATTCGATTAACAAACAAATATTTAA 2233
QY 548 TTACGATTTTATGATTAACCAAAATGCTAAAGTGAAATCCAAAGATCAACACCT 607
DB 2232 TAAATATATTTTAAACCCAAATAATAATAATAAACCCCTAATATATCAACAT 2173
QY 608 ACAGTGA 616
DB 2172 ACACAAAA 2164

RESULT 12

US-09-754-853A-2/c
Sequence 2, Application US/09754853A
Publication No. US20030005491A1
GENERAL INFORMATION:
APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 2
LENGTH: 335913
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: CDS
LOCATION: (45163)..(45314)..(45450)..(45509)..(46941)..(48763)..(48975)..(49573)
OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853A-2

Query Match 3.9%; Score 40; DB 9; Length 335913;

Best Local Similarity 45.5%; Pred. No. 2.7e+02;

Matches 142; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 5 TTCAATGATTAAGTAAATATTTTATGACCAATGATGAGCTTTGTAATGATGATTA 64
DB 280510 TTTTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 280451

QY 65 AAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 124
DB 280450 AAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 280391
QY 125 CATTAACAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 184
DB 280390 AAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 280331
QY 185 GTAATATTTAGGCTGATTTGTTAATTTCTAGAGTCCCAACGCGCATTAACAT 244
DB 280330 ATGAGATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 280271
QY 245 TACAACCTTAACCTTTGTTGTTAATTTCTTAATGAAGAAACCTTAAAGAAATTA 304
DB 280270 AATATTAATCTTTTAAATGACCGCTATTAATTAATTAATTAATTAATTAAT 280211
QY 305 GATGACACAAA 316
DB 280210 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 280199

RESULT 13

US-09-754-853A-3/c
Sequence 3, Application US/09754853A
Publication No. US20030005491A1
GENERAL INFORMATION:
APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 3
LENGTH: 335913
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: CDS
LOCATION: (46798)..(48763)..(48975)..(49573)
OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853A-3

Query Match 3.9%; Score 40; DB 9; Length 335913;

Best Local Similarity 45.5%; Pred. No. 2.7e+02;

Matches 142; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 5 TTCAATGATTAAGTAAATATTTTATGACCAATGATGAGCTTTGTAATGATGATTA 64
DB 280510 TTTTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 280451
QY 65 AAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 124
DB 280450 AAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 280391
QY 125 CATTAACAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 184
DB 280390 AAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 280331
QY 185 GTAATATTTAGGCTGATTTGTTAATTTCTAGAGTCCCAACGCGCATTAACAT 244
DB 280330 ATGAGATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 280271
QY 245 TACAACCTTAACCTTTGTTGTTAATTTCTTAATGAAGAAACCTTAAAGAAATTA 304
DB 280270 AATATTAATCTTTTAAATGACCGCTATTAATTAATTAATTAATTAATTAAT 280211

QY 305 GATAGCACAAA 316
DB 280210 TATATAATTAAA 280199

RESULT 14

US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. US20020127687A1
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEKI
; APPLICANT: HATORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 3.8%; Score 39.8; DB 10; Length 640681;
Best Local Similarity 52.8%; Pred. No. 3.7e+02;
Matches 86; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 56 ATAACTTTAAATATATATCTGTTAGCTTAAAGATATAGGTTATACGATGAGTA 115
DB 527243 ATATCTTTTAAATTTTATTTTATATACATATATGATATCATTTTGCATATGATATA 527302
QY 116 TTTTACGATCATACACGATCGATGATACGAAATATCATATACACGAACTAGA 175
DB 527303 ATCAAAATGTTATCAAAAAATTTTATGATCAAAAAACAAATTTTATCTAAA 527362
QY 176 CACGGAACGTAATTTTATGAGGCTGATGTTGTTATATTTCTA 218
DB 527363 AATTAACACTTTTATGTTAAAAACCTTTTATATATATCTA 527405

RESULT 15

US-09-790-988-1/c
; Sequence 1, Application US/09790988
; Patent No. US20020127687A1
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEKI
; APPLICANT: HATORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 3.8%; Score 39.6; DB 10; Length 640681;
Best Local Similarity 43.5%; Pred. No. 4.1e+02;
Matches 180; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

QY 498 GGAAGATGTAAAACTTATCTAGCGGCTTTTGATATACGAGATGTTCACTTATTT 557

DB 347364 GAAAAACCTTACAGATTCAAAACGTAATTTGCAATTTAAGCATATAGCTTATCAAT 347305
QY 558 TAGATTACCAAAAAATGGCTAAAGTGAAATACCAAAAGATACACACCTTACGTGAAG 617
DB 347304 TATTTAAAGAAACAAAAATATTTAAGAAATAAAAATGAAATGTTAGACATCACTTTATAC 347245
QY 618 TAAAGGTAATGATGATTAAGATAGTATACACTCTGTAATGCAAGTAAATTCATTT 677
DB 347244 AGTCAAGTAAGATTTTAAACGCTCTTAATTTGAATTTATCTTTTAAAGAAAAATAC 347185
QY 678 ACCCTCTGACGTAATTTACTAAGTGAAGAGCAATTTTAAAGGTAATTAAT 737
DB 347184 ATCATTTTCTATGTCATACCTAATTTCTCTGACGATGTTCCAGAGGAAATACAT 347125
QY 738 ATGTTAAGGAAGATACATATCCAGAAATGGGGAGAAAAATCCGATTATAGCCAGAGAC 797
DB 347124 CGATTAAATTAATTAAGAAATTTAAATACCTGGGTCAAAAAAGAGTATGATTTGAAATCC 347065
QY 798 CAGTTTTCATGAAATATTTAAAAAAGATTAAGATGCAACATATATAGTTTACAGATT 857
DB 347064 AAGATCATATAGAGCTAGGAAAAATTTTAAAGATTTAGATTGGAATCTTCTGACAAA 347005
QY 858 TAGTACGTACAAATCAAAAAATGAGTACATCAATGATGTTGTTTCCATG 911
DB 347004 TGTCAAGATCAAGATTTGTTAATGAAGGAAAAATTTCTTTTACACCGTG 346951

Search completed: June 15, 2003, 21:41:34
Job time : 194 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 19:36:31 ; Search time 2746 Seconds

(without alignments)
10958.595 Million cell updates/sec

Title: US-09-976-605-5

Perfect score: 1034

Sequence: 1 aagctcatgataaagtaaa.....agaagacgaaccctcgag 1034

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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40: em_hcgo_mus:*
41: em_hcgo_other:*
  
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

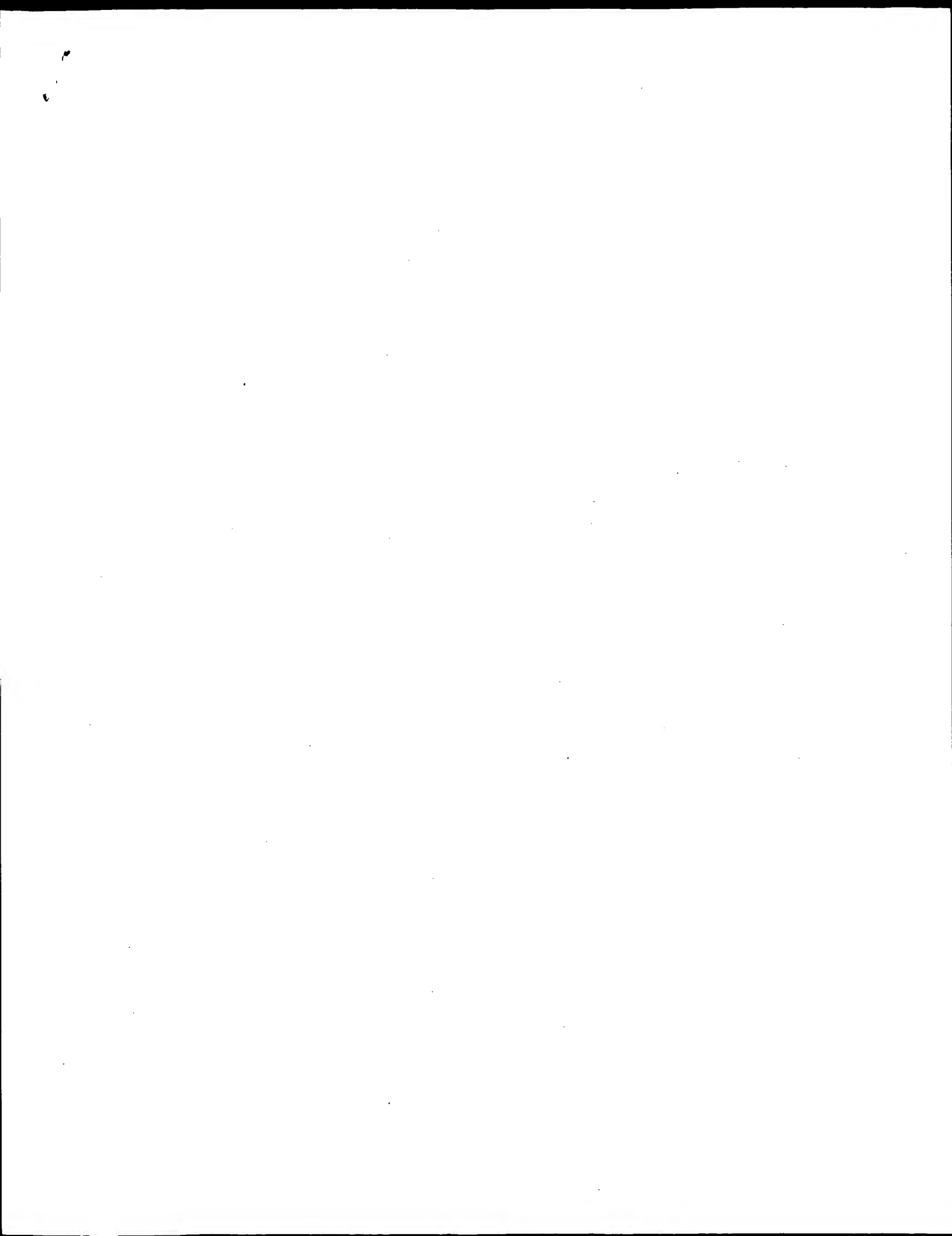
SUMMARIES

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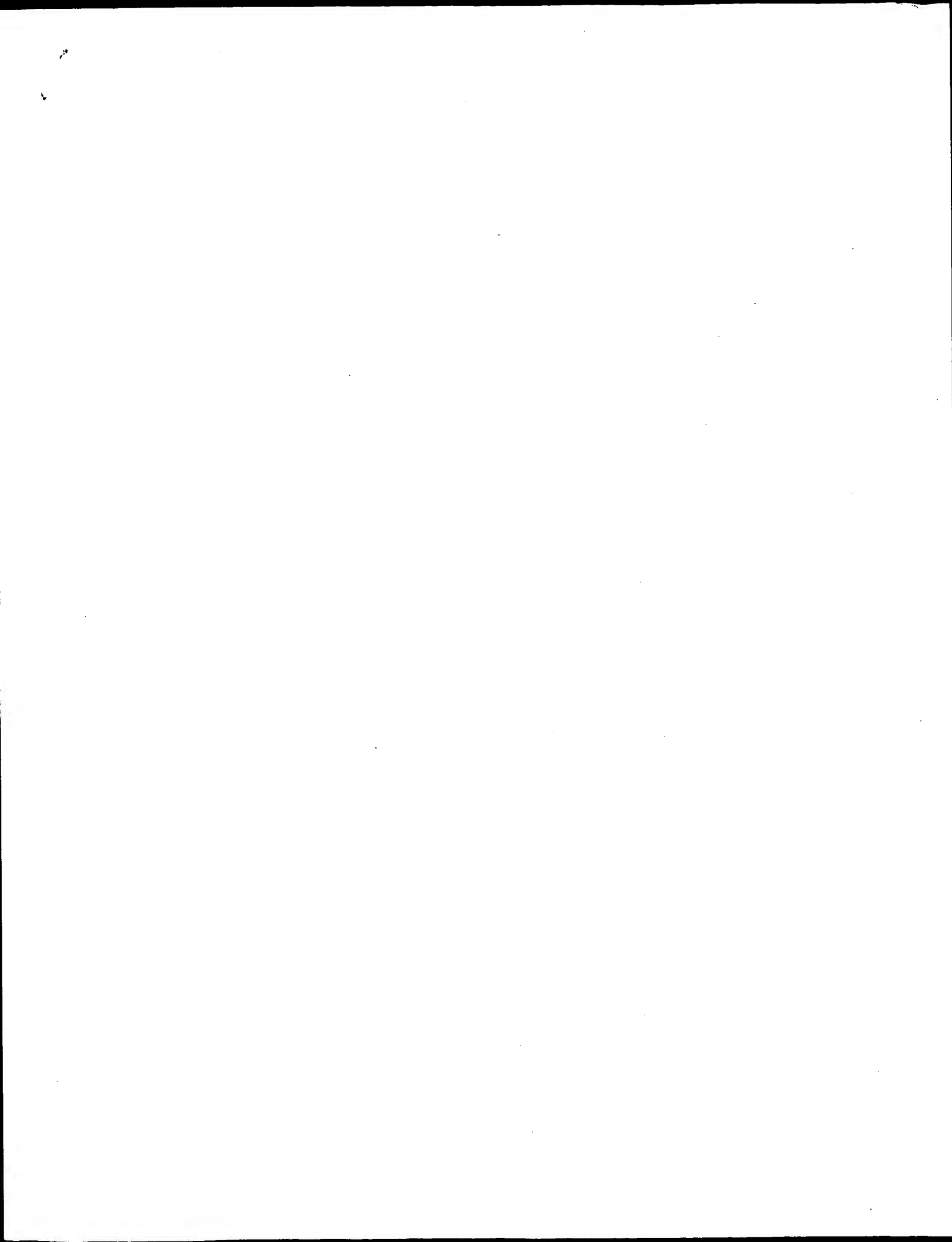
ALIGNMENTS

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DEFINITION Yaba-like disease virus (YLDV), complete genome.
ACCESSION AJ293568
VERSION AJ293568.1 GI:12056159
KEYWORDS 100L gene; 101L gene; 102R gene; 103L gene; 104L gene; 105L gene;
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DB 1866 CC 1865

RESULT 2
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LOCUS ARI45601 1023 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence .53 from patent US 6217882.
ACCESSION ARI45601
VERSION ARI45601.1 GI:15108790
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1023)
AUTHORS Moyer, R.W., Vinuela, E. and Gibbs, E.P.J.
TITLE Use of recombinant swine poxvirus as a live vaccine vector
JOURNAL Patent: US 6217882-A 53 17-Apr-2001;
FEATURES
source location/Qualifiers
BASE COUNT 359 a 158 c 199 g 307 t
ORIGIN

Query Match
Best Local Similarity 12.9%; Score 133.6; DB 6; Length 1023;
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DB 35 TTAGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 94





STIC Search Report

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STIC Database Tracking Number: 96300

TO: Ulrike Winkler
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Art Unit: 1648
Monday, June 16, 2003

Case Serial Number: 976605

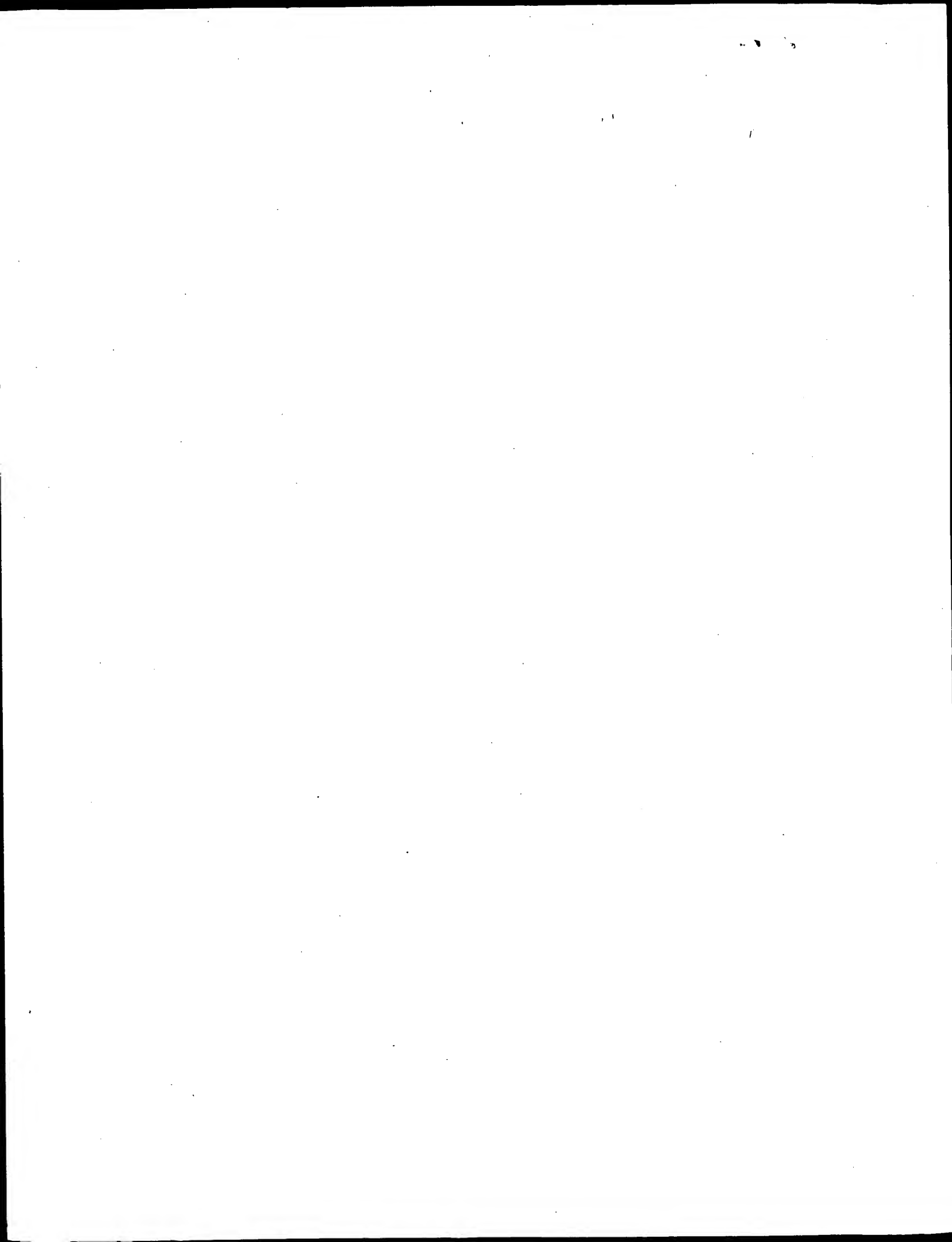
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Please search SEQ ID NO 5 of application 09/976605.

Thanks, Ulrike

Ulrike Winkler, Ph.D.
Patent Examiner
Crystal Mall 1, 8D09/ Mail Box 8E12
1911 South Clark Place
Arlington, VA 22202
tel. 703-308-8294
fax. 703-308-4426

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Date Picked Up: 6/11/03
Date Completed: 6/16/03
Searcher Prep/Review: 3
Clerical: 5
Online time: 5

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
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Other (specify): _____



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Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

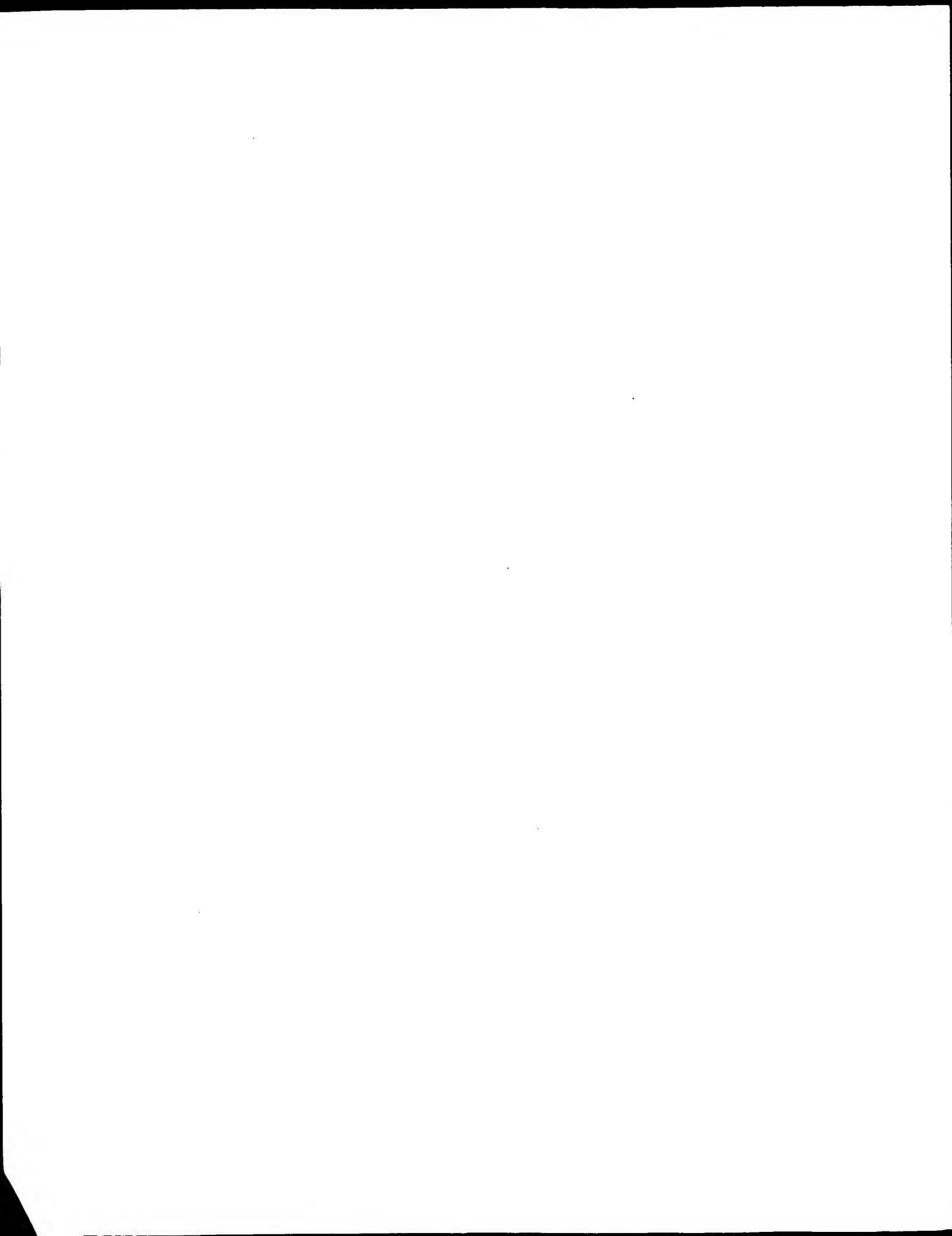
➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

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Thanks, Ulrike

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